GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 22:16:05 ; Search time 1037 Seconds
(without alignments)
703.635 Million cell updates/sec

Title: US-10-070-882A-2
Perfect score: 139
Sequence: 1 gtgactctggtcgacgaact.....ctgttcttattgttaacaca 139

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	139	100.0	139	4	AAF82356	Aaf82356 Salmonell
	2	139	100.0	2802	12	ADG31136	Adg31136 Salmonell
	3	40	28.8	41	6	ABL57265	Abl57265 Escherich
	4	37.2	26.8	1385	8	ACA49482	Aca49482 Prokaryot
	5	32.6	23.5	266145	10	ADE87477	Ade87477 Fowlpox v
c	6	31	22.3	772	6	ABQ72598	Abq72598 Human MDD
c	7	31	22.3	810	6	ABQ72685	Abq72685 Human MDD
c	8	30.8	22.2	19521	4	AAK81193	Aak81193 Human imm
c	9	30.8	22.2	19521	8	ADA41637	Ada41637 Human sec
c	10	30.8	22.2	19521	10	ADA57769	Ada57769 BAC fragm
	11	30.6	22.0	1539	8	ACA02032	Aca02032 C. glutam
	12	30.6	22.0	2799	5	AAH67957	Aah67957 C glutami
c	13	30.6	22.0	349980	5	AAH68533	Aah68533 C glutami
c	14	30.4	21.9	31241	10	AAD63515	Aad63515 Mycoplasm
c	15	30.4	21.9	31241	10	ACC69145	Acc69145 M. genita
c	16	30.4	21.9	31241	12	ADN48950	Adn48950 Mycoplasm
c	17	30.4	21.9	104644	6	ABQ99653	Abq99653 Human MS4
c	18	30.2	21.7	110000	9	ADB12064_03	Continuation (4 of
	19	30	21.6	622	12	ADJ38283	Adj38283 Plastid d
c	20	30	21.6	10711	4	AAK74790	Aak74790 Human imm
	21	29.8	21.4	301	3	AAA06526	Aaa06526 Human imm
	22	29.8	21.4	301	4	AAH93642	Aah93642 Human pro
	23	29.8	21.4	301	4	AAS63734	Aas63734 Human pro
	24	29.8	21.4	301	4	AAH02707	Aah02707 Prostate
	25	29.8	21.4	301	4	AAH84956	Aah84956 Human pro
	26	29.8	21.4	301	5	ACA59543	Aca59543 Prostate
	27	29.8	21.4	301	6	ABL95106	Abl95106 Human P8D
	28	29.8	21.4	301	8	ACC95270	Acc95270 Prostate
	29	29.8	21.4	301	10	ADB13743	Adb13743 Human pro
	30	29.8	21.4	301	10	ADG26159	Adg26159 Human pro
	31	29.8	21.4	340	5	ABV07484	Abv07484 Human pro
	32	29.8	21.4	409	5	ABV37417	Abv37417 Human pro
	33	29.8	21.4	492	6	ABL64736	Abl64736 Lung canc
	34	29.8	21.4	492	6	ABL65652	Abl65652 Lung canc
c	35	29.8	21.4	1140	10	ADC92238	Adc92238 E. faeciu
	36	29.8	21.4	1448	2	AAZ33468	Aaz33468 Human pro
c	37	29.8	21.4	2143	2	AAZ42062	Aaz42062 Human end
	38	29.8	21.4	2654	6	ABS57323	Abs57323 cDNA enco
c	39	29.8	21.4	2700	4	ABL28364	Abl28364 Drosophil
	40	29.8	21.4	2840	12	ADP64619	Adp64619 DNA of hu
	41	29.8	21.4	2962	10	ADB63189	Adb63189 Human cDN
	42	29.8	21.4	3017	4	AAF29360	Aaf29360 Amyloid-b
	43	29.8	21.4	3017	5	AAF93907	Aaf93907 Human cDN
	44	29.8	21.4	3042	8	ACC50169	Acc50169 Breast ca
	45	29.8	21.4	3042	10	ADB75331	Adb75331 Prostate
	46	29.8	21.4	3042	10	ADD18542	Add18542 Human pro
	47	29.8	21.4	3045	4	AAH14672	Aah14672 Human cDN
	48	29.8	21.4	3051	3	AAC64559	Aac64559 Human pro
	49	29.8	21.4	3079	12	ADP64620	Adp64620 DNA of hu
	50	29.8	21.4	3154	6	ABQ99606	Abq99606 Human cod
	51	29.8	21.4	3174	3	AAA26421	Aaa26421 Human sec
	52	29.8	21.4	3174	12	ADL71482	Adl71482 Novel hum
	53	29.8	21.4	3210	5	ABV25476	Abv25476 Human pro
	54	29.8	21.4	4042	8	ABZ35869	Abz35869 Human sec
	55	29.6	21.3	2940	11	ADN95667	Adn95667 Human BEC
	56	29.6	21.3	2941	10	ADD71105	Add71105 Human met
c	57	29.6	21.3	87980	8	AAD53223_4	Continuation (5 of
c	58	29.4	21.2	2087	4	AAH15446	Aah15446 Human cDN
c	59	29.4	21.2	32249	4	AAL04789	Aal04789 Human rep
c	60	29.4	21.2	32249	4	ABL97684	Abl97684 Human tes
c	61	29.4	21.2	43602	6	ABS78851	Abs78851 E. coli C
c	62	29.4	21.2	43602	10	ADH80418	Adh80418 Escherich
c	63	29.2	21.0	720	10	ABX06274	Abx06274 S. pneumo
c	64	29.2	21.0	3000	4	AAD20312	Aad20312 Streptoco
c	65	29.2	21.0	3000	4	AAD20311	Aad20311 Streptoco
c	66	29.2	21.0	16593	2	AAV52185	Aav52185 Streptoco
c	67	29.2	21.0	110000	10	ABS56454_04	Continuation (5 of
	68	29	20.9	3010	3	AAA26920	Aaa26920 Essential
	69	29	20.9	3010	4	AAF91602	Aaf91602 Staphyloc
	70	29	20.9	3010	4	AAS08071	Aas08071 Staphyloc
	71	29	20.9	3010	10	ADD67449	Add67449 Antibacte
	72	29	20.9	3010	10	ADE73673	Ade73673 Mutant ba
c	73	28.6	20.6	485	4	AAI14190	Aai14190 Probe #41
c	74	28.6	20.6	485	4	ABA55917	Aba55917 Human foe
c	75	28.6	20.6	485	4	ABA25583	Aba25583 Probe #40
c	76	28.6	20.6	485	4	ABS29249	Abs29249 Human liv
c	77	28.6	20.6	485	6	ABS04169	Abs04169 Human gen
c	78	28.6	20.6	2673	8	ABZ58100	Abz58100 Mouse inh
c	79	28.6	20.6	2676	2	AAV55042	Aav55042 Murine HI
c	80	28.6	20.6	16397	2	AAV74516	Aav74516 Staphyloc
c	81	28.4	20.4	984	8	ACF74642	Acf74642 Staphyloc
	82	28.4	20.4	1092	3	AAZ51212	Aaz51212 Staphyloc
	83	28.4	20.4	1092	6	AAD42202	Aad42202 Staphyloc
	84	28.4	20.4	1301	12	ADM77936	Adm77936 S. suis A
c	85	28.4	20.4	1320	2	AAT43930	Aat43930 Sequence
c	86	28.4	20.4	1320	2	AAT72050	Aat72050 Sequence
	87	28.4	20.4	2000	10	ACC60950	Acc60950 Gene sequ
	88	28.4	20.4	2000	10	ADK62457	Adk62457 Disease t
	89	28.4	20.4	4676	12	ADM77938	Adm77938 S. suis A
	90	28.4	20.4	5549	2	AAV74499	Aav74499 Staphyloc
c	91	28.2	20.3	145	8	ACC79383	Acc79383 Mouse DST
	92	28.2	20.3	1242	9	ADA30447	Ada30447 DNA encod
c	93	28.2	20.3	1323	10	ACC61275	Acc61275 Gene sequ
c	94	28.2	20.3	1323	10	ADK63695	Adk63695 Disease t

c	95	28.2	20.3	2307	2	AAV43009	Aav43009 Streptoco
c	96	28.2	20.3	2787	2	AAZ96363	Aaz96363 S. pneumo
c	97	28.2	20.3	3005	4	AAD20313	Aad20313 Streptoco
	98	28.2	20.3	3563	10	ADE58284	Ade58284 Human gen
	99	28.2	20.3	3798	2	AAQ42424	Aaq42424 ADA2 DNA.
c	100	28.2	20.3	5311	10	ADD29639	Add29639 Mouse tum

ALIGNMENTS

RESULT 1
AAF82356
ID AAF82356 standard; DNA; 139 BP.
XX
AC AAF82356;
XX
DT 22-JUN-2001 (first entry)
XX
DE Salmonella typhimurium phoP gene promoter.
XX
KW Salmonella typhimurium; phoP gene promoter; PphoP; antibacterial;
KW antiviral; vaccine; lacZ; pagC; outer membrane porin C; ompC;
KW transgenic microorganism; antigen production; antigen delivery;
KW infection; ds.
XX
OS Salmonella typhimurium.
XX
PN WO200119974-A2.
XX
PD 22-MAR-2001.
XX
PF 06-SEP-2000; 2000WO-GB003402.
XX
PR 10-SEP-1999; 99GB-00021275.
PR 12-JUL-2000; 2000GB-00017000.
XX
PA (MINA) UK SEC FOR DEFENCE.
XX
PI Titball RW, Bullifent HL;
XX
DR WPI; 2001-328017/34.
XX
PT New recombinant gut-colonizing microorganism, useful as vaccine
PT component, comprises construct containing phoP, pagC or ompC gene
PT promoter linked to nucleic acid encoding protein that induces immune
PT response against pathogen.
XX
PS Claim 1; Fig 6; 33pp; English.
XX
CC The present sequence is a DNA fragment comprising the phoP gene promoter.
CC DNA fragments comprising the Salmonella typhimurium phoP, pagC and ompC
CC gene promoters were integrated into a vector used to transform a
CC recombinant gut-colonising microorganism. The promoter was operably
CC linked to a nucleic acid encoding a protein that is able to induce a
CC protective immune response against an organism in a mammal. The construct
CC is useful for enhancing expression of a desired protein at mucosal
CC effector sites. It is useful for delivering a variety of antigenic agents
CC which can be used to induce a protective immune response against a wide
CC range of pathogens such as Bacillus anthracis, Bordetella pertussis,
CC Schistoma mansoni, herpes simplex virus, and Mycobacterium tuberculosis.
CC The three promoters (P(phoP), P(pagC) and P(ompC)) are induced at
CC different stages in the infection process, and hence at different sites
CC in the body. This approach allows the induction of different immune
CC responses which provide protection against pathogens which colonise
CC different host cell compartments. The Salmonella vaccine vector system is
CC ideally suited to the delivery of many vaccine antigens since the vaccine
CC delivery mechanism accurately mimics the natural disease, entering the
CC body via the gut
XX
SQ Sequence 139 BP; 37 A; 33 C; 23 G; 46 T; 0 U; 0 Other;

Query Match 100.0%; Score 139; DB 4; Length 139;
Best Local Similarity 100.0%; Pred. No. 5.6e-36;
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGG 60

Qy         61 GTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGAC 120

Qy        121 TGTTCTTATTGTTAACACA 139
              ||||||||||||||||||
Db        121 TGTTCTTATTGTTAACACA 139
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RESULT 2
ADG31136
ID ADG31136 standard; DNA; 2802 BP.
XX
AC ADG31136;
XX
DT 26-FEB-2004 (first entry)
XX
DE Salmonella typhimurium PphoPQ and phoPQ operon DNA.
XX
KW live attenuated derivative; pathogenic Enterobacteriaceae;
KW cross protective immunity; antibacterial; immunostimulant; vaccine;
KW PphoPQ; promoter; phoPQ operon; ds; gene.
XX
OS Salmonella typhimurium.
XX
PN WO2003096812-A1.
XX
PD 27-NOV-2003.
XX
PF 15-APR-2003; 2003WO-US011802.
XX
PR 15-APR-2002; 2002US-0372616P.
PR 18-APR-2002; 2002US-0373626P.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Curtiss R;
XX
DR WPI; 2004-042484/04.
DR P-PSDB; ADG31137, ADG31138, ADG31139.
XX
PT New live attenuated derivative of a pathogenic Enterobacteriaceae
PT species, useful as a vaccine for inducing cross protective immunity
PT against infections caused by various Enterobacteriaceae strains or
PT serotypes.
XX
PS Example 17; Fig 28; 133pp; English.
XX
CC The invention relates to a novel live attenuated derivative of a
CC pathogenic Enterobacteriaceae species having enhanced ability to induce
CC cross protective immunity against Enterobacteriaceae. The derivative of
CC the invention demonstrates antibacterial and immunostimulant activities
CC and may be useful as a vaccine for inducing a high level immune response
CC and/or cross protective immune response to protect individuals from
CC infection from a diversity of species or serotypes of bacterial
CC pathogens. The current sequence is that of the Salmonella typhimurium
CC PphoPQ and phoPQ operon DNA of the invention.
XX
SQ Sequence 2802 BP; 721 A; 702 C; 724 G; 655 T; 0 U; 0 Other;

Query Match 100.0%; Score 139; DB 12; Length 2802;
Best Local Similarity 100.0%; Pred. No. 1.3e-35;
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        511 GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGG 570

Qy         61 GTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 GTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGAC 630

Qy        121 TGTTCTTATTGTTAACACA 139
              ||||||||||||||||||
Db        631 TGTTCTTATTGTTAACACA 649


RESULT 3
ABL57265
ID   ABL57265 standard; DNA; 41 BP.
XX
AC   ABL57265;
XX
DT   09-AUG-2002  (first entry)
XX
DE   Escherichia coli DNA 5' to phoA coding region.
XX
KW   Transcription terminator; trpA; attenuation; vaccine; virucide;
KW   antibacterial; fungicide; antiparasitic; protozoacide; phoA; ds.
XX
OS   Escherichia coli.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .19
FT                   /*tag=  a
FT                   /note= "5' single-stranded overhang"
FT   misc_feature    41
FT                   /*tag=  b
FT                   /note= "5' overhang on complementary strand of 4 bases
FT                   with sequence 5'-GATC-3'"
XX
PN   WO200230457-A2.
XX
PD   18-APR-2002.
XX
PF   11-OCT-2001; 2001WO-US031606.
XX
PR   12-OCT-2000; 2000US-00689123.
XX
PA   (UNIW ) UNIV WASHINGTON.
PA   (MEGA-) MEGAN HEALTH INC.
PA   (CURT/) CURTISS R.
PA   (TING/) TINGE S A.
XX
PI   Curtiss R,  Tinge SA;
XX
DR   WPI; 2002-444150/47.
XX
PT   Composition comprising microbe having attenuating mutation that comprises
PT   insertion sequence containing recombinant transcription terminator,
PT   useful as vaccine, and for delivering a desired gene product to
PT   individual.
XX
PS   Example 5; Fig 11; 91pp; English.
XX
CC   The present sequence is that of DNA located 5' to the phoA coding
CC   sequence of Escherichia coli. The sequence was used to illustrate an
CC   example of the invention relating to deletion of the phoA gene and
CC   replacement with a trpA terminator. The phoA mutation was introduced into
CC   Salmonella typhimurium SL1344 to produce strain MGN-1362. The present
CC   invention is based on the discovery that transcription terminators (TTs)
CC   can be inserted in a bacterial gene in an attenuating strategy which not
CC   only attenuates the virulence of the bacteria, but also serves to
CC   restrict the effect of the attenuating mutation to the target gene or
CC   operon of the bacteria. A claimed vaccine comprises a microorganism
CC   having an attenuating mutation in a chromosomal gene, the mutation
CC   comprising an insertion sequence which contains a recombinant TT, such as
CC   trpA. The microorganism is preferably Salmonella, Shigella or
CC   Escherichia, and the TT is preferably inserted in the phoP gene. The
CC   vaccine may further comprise a recombinant gene encoding a desired gene
CC   product from a virus, bacterium, protozoan, parasite or fungus, or
CC   encodes an autoantigen, gamete-specific antigen or an allergen. The
CC   attenuated microorganism is also used in a claimed method for delivering
CC   a desired gene product to an individual
XX
SQ   Sequence 41 BP; 10 A; 13 C; 4 G; 14 T; 0 U; 0 Other;

  Query Match            28.8%;  Score 40;  DB 6;  Length 41;
  Best Local Similarity  100.0%;  Pred. No. 0.0021;
  Matches   40;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTT 50
              |||||||||||||||||||||||||||||||||||||||
Db          1 TCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTT 40


RESULT 4
ACA49482
ID   ACA49482 standard; DNA; 1385 BP.
XX
AC   ACA49482;
XX
DT   19-JUN-2003  (first entry)
XX
DE   Prokaryotic essential gene #31139.
XX
KW   Antisense; ds; prokaryotic essential gene; cell proliferation;
KW   drug design; gene.
XX
OS   Salmonella paratyphi.
XX
PN   WO200277183-A2.
XX
PD   03-OCT-2002.
XX
PF   21-MAR-2002; 2002WO-US009107.
XX
PR   21-MAR-2001; 2001US-00815242.
PR   06-SEP-2001; 2001US-00948993.
PR   25-OCT-2001; 2001US-0342923P.
PR   08-FEB-2002; 2002US-00072851.
PR   06-MAR-2002; 2002US-0362699P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Wang L,  Zamudio C,  Malone C,  Haselbeck R,  Ohlsen KL,  Zyskind JW;
PI   Wall D,  Trawick JD,  Carr GJ,  Yamamoto R,  Forsyth RA,  Xu HH;
XX
DR   WPI; 2003-029926/02.
DR   P-PSDB; ABU45612.
XX
PT   New antisense nucleic acids, useful for identifying proteins or screening
PT   for homologous nucleic acids required for cellular proliferation to
PT   isolate candidate molecules for rational drug discovery programs.
XX
PS   Claim 14; SEQ ID NO 37352; 1766pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising any one of
CC   the 6213 antisense sequences given in the specification where expression
CC   of the nucleic acid inhibits proliferation of a cell. Also included are:
CC   (1) a vector comprising a promoter operably linked to the nucleic acid
CC   encoding a polypeptide whose expression is inhibited by the antisense
CC   nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC   polypeptide or its fragment whose expression is inhibited by the
CC   antisense nucleic acid; (4) an antibody capable of specifically binding
CC   the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC   proliferation or the activity of a gene in an operon required for
CC   proliferation; (7) identifying a compound that influences the activity of
CC   the gene product or that has an activity against a biological pathway
CC   required for proliferation, or that inhibits cellular proliferation; (8)
CC   identifying a gene required for cellular proliferation or the biological
CC   pathway in which a proliferation-required gene or its gene product lies
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CC   or a gene on which the test compound that inhibits proliferation of an
CC   organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC   compound's activity; (11) a culture comprising strains in which the gene
CC   product is overexpressed or underexpressed; (12) determining the extent
CC   to which each of the strains is present in a culture or collection of
CC   strains; or (13) identifying the target of a compound that inhibits the
CC   proliferation of an organism. The antisense nucleic acids are useful for
CC   identifying proteins or screening for homologous nucleic acids required
CC   for cellular proliferation to isolate candidate molecules for rational
CC   drug discovery programs, or for screening homologous nucleic acids
CC   required for proliferation in cells other than S. aureus, S. typhimurium,
CC   K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC   prokaryotic essential genes. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1385 BP; 353 A; 372 C; 335 G; 321 T; 0 U; 4 Other;

  Query Match             26.8%;  Score 37.2;  DB 8;  Length 1385;
  Best Local Similarity   92.9%;  Pred. No. 0.048;
  Matches   39;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCT 42
              |||||||||||||||||||||||||||||   ||||||||||
Db       1344 GTGACTCTGGTCGACGAACTTAAATAATATGTGCCTCACCCT 1385


RESULT 5
ADE87477
ID   ADE87477 standard; DNA; 266145 BP.
XX
AC   ADE87477;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Fowlpox virus genome DNA.
XX
KW   fowlpox virus; FPV; virucide; tuberculostatic; protozoacide; antipyretic;
KW   cytostatic; hepatotropic; antibacterial; vaccine; malaria; tuberculosis;
KW   East Coast fever; avipox virus; influenza; hepatitis;
KW   human papilloma virus; tumour; leishmaniasis; listeriosis; theileria;
KW   gene; ds.
XX
OS   Fowlpox virus.
XX
PN   WO2003047617-A2.
XX
PD   12-JUN-2003.
XX
PF   02-DEC-2002; 2002WO-GB005411.
XX
PR   30-NOV-2001; 2001GB-00028733.
PR   30-NOV-2001; 2001US-0334649P.
XX
PA   (ISIS-) ISIS INNOVATION LTD.
XX
PI   Laidlaw S,  Skinner M,  Hill A,  Gilbert S,  Anderson R;
XX
DR   WPI; 2003-513700/48.
XX
PT   Treating and/or preventing e.g. malaria or tuberculosis, or eliciting an
PT   immune response, comprises administering a priming composition and a
PT   boosting composition containing a non-replicating viral vector in either
PT   order.
XX
PS   Claim 30; SEQ ID NO 1; 302pp; English.
XX
CC   The invention relates to a fowlpox virus (FPV) genome which has
CC   modifications in one or more wild-type FPV genes. The invention further
CC   relates to a novel method for treating and/or preventing a disease in a
CC   subject comprising administering two compositions, each containing a non-
CC   replicating viral vector. At least one of the compositions comprises a
CC   poxvirus vector derived from a fowlpox virus. The novel compositions have
CC   the following activities: virucide, tuberculostatic, protozoacide,
CC   antipyretic, cytostatic, hepatotropic, and antibacterial. The non-
CC   replicating viral vector is useful in a vaccine for an animal,
CC   particularly a mammal such as a primate, specifically human. The priming
CC   or boosting composition, or the kit is useful for manufacturing a
CC   medicament for treating and/or preventing a disease which is, or results
CC   from, a chronic infection such as malaria, tuberculosis or East Coast
CC   fever, or for eliciting a T-cell immune response in a subject. Non-
CC   cultured CEF cells are useful for growing an avipox virus, such as
CC   fowlpox virus. The method or the vaccine may further be used to treat or
CC   prevent influenza, hepatitis, human papilloma virus and other viral
CC   infections, malignancies such as tumours, leishmaniasis, listeriosis, and
CC   theileria. This polynucleotide sequence represents the DNA of the fowlpox
CC   virus genome of the invention.
XX
SQ   Sequence 266145 BP; 92375 A; 41026 C; 40846 G; 91897 T; 0 U; 1 Other;

  Query Match             23.5%;  Score 32.6;  DB 10;  Length 266145;
  Best Local Similarity   55.9%;  Pred. No. 7;
  Matches   62;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

Qy         18 ACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGT 77
              | |||  ||  |      | |   |||| ||  | ||| || |  ||    | || ||
Db      21181 AGTTACTTATAGATATATTTAATATCTTATCGACGGAAGGACGAAGATCCATGGTATGTG 21240

Qy         78 TTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTTA 128
              |||| |  | | | |||  ||||    || |||||  ||| | |||| |||
Db      21241 TTATGATGTTTCTGTCCATAAAGGGTAATGATCAATACTATAATGTTTTTA 21291


RESULT 6
ABQ72598/c
ID   ABQ72598 standard; cDNA; 772 BP.
XX
AC   ABQ72598;
XX
DT   03-SEP-2002  (first entry)
XX
DE   Human MDDT encoding cDNA SEQ ID NO 150.
XX
KW   Human; MDDT; disease detection and treatment molecule polynucleotide;
KW   proliferative disorder; hepatitis; psoriasis; cancer; AIDS;
KW   autoimmune disorder; inflammatory disorder; allergy; multiple sclerosis;
KW   rheumatoid arthritis; transgenic; gene therapy; antiarteriosclerotic;
KW   hepatotropic; antiinflammatory; antipsoriatic; cytostatic; anti-HIV;
KW   antiallergic; antianaemic; antiasthmatic; antiatherosclerotic; antigout;
KW   neuroprotective; antirheumatic; antiarthritic; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200240715-A2.
XX
PD   23-MAY-2002.
XX
PF   06-SEP-2001; 2001WO-US027628.
XX
PR   05-SEP-2000; 2000US-0229747P.
PR   05-SEP-2000; 2000US-0229748P.
PR   05-SEP-2000; 2000US-0229749P.
PR   05-SEP-2000; 2000US-0229750P.
PR   05-SEP-2000; 2000US-0229751P.
PR   05-SEP-2000; 2000US-0230583P.
PR   06-SEP-2000; 2000US-0230505P.
PR   06-SEP-2000; 2000US-0230514P.
PR   06-SEP-2000; 2000US-0230515P.
PR   06-SEP-2000; 2000US-0230517P.
PR   06-SEP-2000; 2000US-0230518P.
PR   06-SEP-2000; 2000US-0230519P.
PR   06-SEP-2000; 2000US-0230595P.
PR   06-SEP-2000; 2000US-0230597P.
PR   06-SEP-2000; 2000US-0230598P.
PR   06-SEP-2000; 2000US-0230599P.
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PR 06-SEP-2000; 2000US-0230610P.
PR 06-SEP-2000; 2000US-0230865P.
PR 06-SEP-2000; 2000US-0230988P.
PR 06-SEP-2000; 2000US-0230989P.
PR 07-SEP-2000; 2000US-0230951P.
PR 07-SEP-2000; 2000US-0231163P.
PR 07-SEP-2000; 2000US-0231167P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Jackson S, Lincoln SE, Altus CM, Dufour GE, Chalup MS;
PI Hillman JL, Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE;
PI Dahl CR, Momiyama MG, Bradley DL, Rohatgi SD, Harris B;
PI Roseberry AM, Gerstin EH, Peralta CH, David MH, Panzer SR, Flores V;
PI Daffo A, Marwaha R, Chen AJ, Chang SC, Au AP, Inman RR;
XX
DR WPI; 2002-527544/56.
DR P-PSDB; ABP51381.
XX
PT Novel human disease detection and treatment polypeptide, useful in
PT diagnosis, prevention or treatment of cell proliferative disorders e.g.
PT arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder e.g.
PT AIDS.
XX
PS Claim 1; Page 390-391; 618pp; English.
XX
CC The invention relates to an isolated human disease detection and
CC treatment (MDDT) polypeptide (I) selected from a polypeptide having a
CC sequence selected from 254 sequences (ABP51231-ABP51484) given in the
CC specification, a naturally occurring polypeptide comprising a sequence
CC having at least 90% identity to (I) or a biologically active or
CC immunogenic fragment of (I). (I) is useful for screening a compound for
CC effectiveness as an agonist or antagonist, for screening a compound that
CC specifically binds (I) or modulates the activity of (I), and for
CC preparing a polyclonal or monoclonal antibody by hybridoma technology.
CC Nucleic acids (II) (ABQ72449-ABQ72700) encoding (I) are useful for
CC screening a compound for effectiveness in altering expression of a target
CC polynucleotide comprising. Oligonucleotides and antibodies are useful for
CC detecting MDDT in a sample or for assessing toxicity of a test compound,
CC in a diagnostic test for a condition or a disease associated with the
CC expression of MDDT in a biological sample, for detecting (I) in a sample,
CC and for purifying (I) from a sample. A composition comprising (I), an
CC agonist or antagonist is useful for treating a disease or condition
CC associated with decreased or increased expression of functional MDDT. (I)
CC or (II) are useful for diagnosing, treating or preventing disorders
CC associated with aberrant expression of MDDT, where the disorders are
CC selected from a cell proliferative disorder such as arteriosclerosis,
CC cirrhosis, hepatitis, psoriasis, and cancer and an
CC autoimmune/inflammatory disorder such as AIDS, Addison's disease,
CC allergy, anaemia, asthma, atherosclerosis, gout, multiple sclerosis or
CC rheumatoid arthritis. (II) are useful for creating knockin humanised
CC animals or transgenic animals to model human diseases, in somatic or
CC germline gene therapy, to generate a transcript image of a tissue or cell
CC type, for detecting differences in the chromosomal location due to
CC translocation or inversion among normal, carrier or affected individuals
CC and as hybridisation probes for mapping naturally occurring genomic
CC sequences
XX
SQ Sequence 772 BP; 252 A; 147 C; 156 G; 217 T; 0 U; 0 Other;

Query Match 22.3%; Score 31; DB 6; Length 772;
Best Local Similarity 57.9%; Pred. No. 4.5;
Matches 55; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 45 TTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACC 104
|| | | ||| | | | |||| | ||| | || |||| || ||||| |
Db 549 TTCCAATAAAAAAAAAGTCCTCCATTTAGTTTATTTTATCACAGTTTTGTCCAAAAGCGCT 490

Qy 105 ATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
| || |||||| ||| | ||| ||||||
Db 489 TTCTGTAATGCTAGAAATCTCTCAGTGTCAACACA 455

RESULT 7
ABQ72685/c
ID ABQ72685 standard; cDNA; 810 BP.
XX
AC ABQ72685;
XX
DT 03-SEP-2002 (first entry)
XX
DE Human MDDT encoding cDNA SEQ ID NO 237.
XX
KW Human; MDDT; disease detection and treatment molecule polynucleotide;
KW proliferative disorder; hepatitis; psoriasis; cancer; AIDS;
KW autoimmune disorder; inflammatory disorder; allergy; multiple sclerosis;
KW rheumatoid arthritis; transgenic; gene therapy; antiarteriosclerotic;
KW hepatotropic; antiinflammatory; antipsoriatic; cytostatic; anti-HIV;
KW antiallergic; antianaemic; antiasthmatic; antiatherosclerotic; antigout;
KW neuroprotective; antirheumatic; antiarthritic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200240715-A2.
XX
PD 23-MAY-2002.
XX
PF 06-SEP-2001; 2001WO-US027628.
XX
PR 05-SEP-2000; 2000US-0229747P.
PR 05-SEP-2000; 2000US-0229748P.
PR 05-SEP-2000; 2000US-0229749P.
PR 05-SEP-2000; 2000US-0229750P.
PR 05-SEP-2000; 2000US-0229751P.
PR 05-SEP-2000; 2000US-0230583P.
PR 06-SEP-2000; 2000US-0230505P.
PR 06-SEP-2000; 2000US-0230514P.
PR 06-SEP-2000; 2000US-0230515P.
PR 06-SEP-2000; 2000US-0230517P.
PR 06-SEP-2000; 2000US-0230518P.
PR 06-SEP-2000; 2000US-0230519P.
PR 06-SEP-2000; 2000US-0230595P.
PR 06-SEP-2000; 2000US-0230597P.
PR 06-SEP-2000; 2000US-0230598P.
PR 06-SEP-2000; 2000US-0230599P.
PR 06-SEP-2000; 2000US-0230610P.
PR 06-SEP-2000; 2000US-0230865P.
PR 06-SEP-2000; 2000US-0230988P.
PR 06-SEP-2000; 2000US-0230989P.
PR 07-SEP-2000; 2000US-0230951P.
PR 07-SEP-2000; 2000US-0231163P.
PR 07-SEP-2000; 2000US-0231167P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Jackson S, Lincoln SE, Altus CM, Dufour GE, Chalup MS;
PI Hillman JL, Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE;
PI Dahl CR, Momiyama MG, Bradley DL, Rohatgi SD, Harris B;
PI Roseberry AM, Gerstin EH, Peralta CH, David MH, Panzer SR, Flores V;
PI Daffo A, Marwaha R, Chen AJ, Chang SC, Au AP, Inman RR;
XX
DR WPI; 2002-527544/56.
DR P-PSDB; ABP51469.
XX
PT Novel human disease detection and treatment polypeptide, useful in
PT diagnosis, prevention or treatment of cell proliferative disorders e.g.
PT arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder e.g.
PT AIDS.
XX
PS Claim 1; Page 435; 618pp; English.
XX
CC The invention relates to an isolated human disease detection and
CC treatment (MDDT) polypeptide (I) selected from a polypeptide having a
CC sequence selected from 254 sequences (ABP51231-ABP51484) given in the
CC specification, a naturally occurring polypeptide comprising a sequence
CC having at least 90% identity to (I) or a biologically active or

```
CC   immunogenic fragment of (I). (I) is useful for screening a compound for
CC   effectiveness as an agonist or antagonist, for screening a compound that
CC   specifically binds (I) or modulates the activity of (I), and for
CC   preparing a polyclonal or monoclonal antibody by hybridoma technology.
CC   Nucleic acids (II) (ABQ72449-ABQ72700) encoding (I) are useful for
CC   screening a compound for effectiveness in altering expression of a target
CC   polynucleotide comprising. Oligonucleotides and antibodies are useful for
CC   detecting MDDT in a sample or for assessing toxicity of a test compound,
CC   in a diagnostic test for a condition or a disease associated with the
CC   expression of MDDT in a biological sample, for detecting (I) in a sample,
CC   and for purifying (I) from a sample. A composition comprising (I), an
CC   agonist or antagonist is useful for treating a disease or condition
CC   associated with decreased or increased expression of functional MDDT. (I)
CC   or (II) are useful for diagnosing, treating or preventing disorders
CC   associated with aberrant expression of MDDT, where the disorders are
CC   selected from a cell proliferative disorder such as arteriosclerosis,
CC   cirrhosis, hepatitis, psoriasis, and cancer and an
CC   autoimmune/inflammatory disorder such as AIDS, Addison's disease,
CC   allergy, anaemia, asthma, atherosclerosis, gout, multiple sclerosis or
CC   rheumatoid arthritis. (II) are useful for creating knockin humanised
CC   animals or transgenic animals to model human diseases, in somatic or
CC   germline gene therapy, to generate a transcript image of a tissue or cell
CC   type, for detecting differences in the chromosomal location due to
CC   translocation or inversion among normal, carrier or affected individuals
CC   and as hybridisation probes for mapping naturally occurring genomic
CC   sequences
XX
SQ   Sequence 810 BP; 262 A; 153 C; 165 G; 230 T; 0 U; 0 Other;

  Query Match            22.3%;  Score 31;  DB 6;  Length 810;
  Best Local Similarity  57.9%;  Pred. No. 4.6;
  Matches   55;  Conservative    0;  Mismatches   40;  Indels    0;  Gaps    0;

Qy         45 TTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACC 104
              || |   | ||| | |   | ||||   |  |||  | || ||||   || ||||| |
Db        549 TTCCAATAAAAAAAAGTCCTCCATTTAGTTTATTTTATCACAGTTTTGTCCAAAAGCGCT 490

Qy        105 ATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
                |    || ||||||    ||| | ||| ||||||
Db        489 TTCTGTAATGCTAGAAATCTCTCAGTGTCAACACA 455


RESULT 8
AAK81193/c
ID   AAK81193 standard; DNA; 19521 BP.
XX
AC   AAK81193;
XX
DT   07-NOV-2001  (first entry)
XX
DE   Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36005.
XX
KW   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW   cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS   Homo sapiens.
XX
PN   WO200157182-A2.
XX
PD   09-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001354.
XX
PR   31-JAN-2000; 2000US-0179065P.
PR   04-FEB-2000; 2000US-0180628P.
PR   24-FEB-2000; 2000US-0184664P.
PR   02-MAR-2000; 2000US-0186350P.
PR   16-MAR-2000; 2000US-0189874P.
PR   17-MAR-2000; 2000US-0190076P.
PR   18-APR-2000; 2000US-0198123P.
PR   19-MAY-2000; 2000US-0205515P.
PR   07-JUN-2000; 2000US-0209467P.
PR   28-JUN-2000; 2000US-0214886P.
PR   30-JUN-2000; 2000US-0215135P.
PR   07-JUL-2000; 2000US-0216647P.
PR   07-JUL-2000; 2000US-0216880P.
PR   11-JUL-2000; 2000US-0217487P.
PR   11-JUL-2000; 2000US-0217496P.
PR   14-JUL-2000; 2000US-0218290P.
PR   26-JUL-2000; 2000US-0220963P.
PR   26-JUL-2000; 2000US-0220964P.
PR   14-AUG-2000; 2000US-0224518P.
PR   14-AUG-2000; 2000US-0224519P.
PR   14-AUG-2000; 2000US-0225213P.
PR   14-AUG-2000; 2000US-0225214P.
PR   14-AUG-2000; 2000US-0225266P.
PR   14-AUG-2000; 2000US-0225267P.
PR   14-AUG-2000; 2000US-0225268P.
PR   14-AUG-2000; 2000US-0225270P.
PR   14-AUG-2000; 2000US-0225447P.
PR   14-AUG-2000; 2000US-0225757P.
PR   14-AUG-2000; 2000US-0225758P.
PR   14-AUG-2000; 2000US-0225759P.
PR   18-AUG-2000; 2000US-0226279P.
PR   22-AUG-2000; 2000US-0226681P.
PR   22-AUG-2000; 2000US-0226868P.
PR   22-AUG-2000; 2000US-0227182P.
PR   23-AUG-2000; 2000US-0227009P.
PR   30-AUG-2000; 2000US-0228924P.
PR   01-SEP-2000; 2000US-0229287P.
PR   01-SEP-2000; 2000US-0229343P.
PR   01-SEP-2000; 2000US-0229344P.
PR   01-SEP-2000; 2000US-0229345P.
PR   05-SEP-2000; 2000US-0229509P.
PR   05-SEP-2000; 2000US-0229513P.
PR   06-SEP-2000; 2000US-0230437P.
PR   06-SEP-2000; 2000US-0230438P.
PR   08-SEP-2000; 2000US-0231242P.
PR   08-SEP-2000; 2000US-0231243P.
PR   08-SEP-2000; 2000US-0231244P.
PR   08-SEP-2000; 2000US-0231413P.
PR   08-SEP-2000; 2000US-0231414P.
PR   08-SEP-2000; 2000US-0232080P.
PR   08-SEP-2000; 2000US-0232081P.
PR   12-SEP-2000; 2000US-0231968P.
PR   14-SEP-2000; 2000US-0232397P.
PR   14-SEP-2000; 2000US-0232398P.
PR   14-SEP-2000; 2000US-0232399P.
PR   14-SEP-2000; 2000US-0232400P.
PR   14-SEP-2000; 2000US-0232401P.
PR   14-SEP-2000; 2000US-0233063P.
PR   14-SEP-2000; 2000US-0233064P.
PR   14-SEP-2000; 2000US-0233065P.
PR   21-SEP-2000; 2000US-0234223P.
PR   21-SEP-2000; 2000US-0234274P.
PR   25-SEP-2000; 2000US-0234997P.
PR   25-SEP-2000; 2000US-0234998P.
PR   26-SEP-2000; 2000US-0235484P.
PR   27-SEP-2000; 2000US-0235834P.
PR   27-SEP-2000; 2000US-0235836P.
PR   29-SEP-2000; 2000US-0236327P.
PR   29-SEP-2000; 2000US-0236367P.
PR   29-SEP-2000; 2000US-0236368P.
PR   29-SEP-2000; 2000US-0236369P.
PR   29-SEP-2000; 2000US-0236370P.
PR   02-OCT-2000; 2000US-0236802P.
PR   02-OCT-2000; 2000US-0237037P.
PR   02-OCT-2000; 2000US-0237038P.
PR   02-OCT-2000; 2000US-0237039P.
PR   02-OCT-2000; 2000US-0237040P.
PR   13-OCT-2000; 2000US-0239935P.
PR   13-OCT-2000; 2000US-0239937P.
PR   20-OCT-2000; 2000US-0240960P.
PR   20-OCT-2000; 2000US-0241221P.
PR   20-OCT-2000; 2000US-0241785P.
PR   20-OCT-2000; 2000US-0241786P.
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PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-483426/52.
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
PS Disclosure; SEQ ID NO 36005; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 19521 BP; 5672 A; 3465 C; 3902 G; 6482 T; 0 U; 0 Other;

Query Match 22.2%; Score 30.8; DB 4; Length 19521;
Best Local Similarity 63.5%; Pred. No. 13;
Matches 47; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 1 GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGG 60
Db 1311 GTAACTCTGGGCAACTTACATAAACTCTCTGTGCCTCAGCTTCTGCACCTGAGAAAAGGG 1252

Qy 61 GTGACTATTTGTCT 74
Db 1251 CTAACAATTCCTAT 1238

RESULT 9
ADA41637/c
ID ADA41637 standard; DNA; 19521 BP.
XX
AC ADA41637;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted protein related DNA.
XX
KW Human; secreted protein; cancer; hyperproliferative disorder;
KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
KW anaemia; allergic reaction; asthma; cardiovascular disorder;
KW wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;
KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW vulnerary; cardiant; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO2002102993-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008123.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-175238/17.
XX
PT New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing,
PT preventing or treating cancer or other hyperproliferative disorder,
PT asthma, allergies or AIDS.
XX
PS Disclosure; SEQ ID NO 2020; 3205pp; English.
XX
CC The invention relates to novel genes ADA39629-ADA40565 and proteins
CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,
CC treating or ameliorating medical conditions e.g. by protein or gene
CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
CC fragments, and agonists or antagonists that bind to the polypeptide are
CC useful for preparing a diagnostic or pharmaceutical composition for

CC diagnosing or treating cancer or other hyperproliferative disorder. The
CC polypeptides and nucleic acid molecules are also useful for detecting,
CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
CC or other hyperproliferative disorders including neoplasms, autoimmune
CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
CC thrombocytopenia), allergic reactions including asthma or eczema,
CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
CC fungal or viral infections including HIV/AIDS), or wound healing and
CC disorders of epithelial cell proliferation. The nucleic acids are also
CC useful for chromosome identification, radiation hybrid mapping or long-
CC range restriction mapping, as molecular weight markers, or as
CC hybridization or diagnostic probes. The polypeptides and antibodies are
CC useful for providing immunological probes for differential identification
CC of the tissues immunohistochemistry assays. The sequences given in
CC ADA40803-ADA41665 represent DNA sequences related to human secreted
CC proteins. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 19521 BP; 5672 A; 3465 C; 3902 G; 6482 T; 0 U; 0 Other;

Query Match 22.2%; Score 30.8; DB 8; Length 19521;
Best Local Similarity 63.5%; Pred. No. 13;
Matches 47; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 1 GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGG 60
|| ||||||| | || || |||| | ||||||| | ||| | | ||||| ||
Db 1311 GTAACTCTGGGCAACTTACATAAACTCTCTGTGCCTCAGCTTCTGCACCTGAGAAAAGGG 1252

Qy 61 GTGACTATTTGTCT 74
| || ||| | |
Db 1251 CTAACAATTCCTAT 1238

RESULT 10
ADA57769/c
ID ADA57769 standard; DNA; 19521 BP.
XX
AC ADA57769;
XX
DT 20-NOV-2003 (first entry)
XX
DE BAC fragment containing human secreted protein gene #505.
XX
KW immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
KW cytostatic; cerebroprotective; neuroprotective; nootropic;
KW cardiovascular; antiarteriosclerotic; gene therapy;
KW human secreted protein; immune disorder; inflammation;
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW triple helix formation; antisense gene therapy; forensic biology; ds;
KW gene; bacterial artificial chromosome.
XX
OS Homo sapiens.
XX
PN WO2002102994-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008278.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-167512/16.
XX
PT New human secreted polypeptides and polynucleotides, useful for
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
PT conditions, respiratory disorders, cancers, CNS disorders, or
PT neurodegenerative disorders.
XX
PS Disclosure; SEQ ID NO 1962; 1754pp; English.
XX
CC The invention relates to 592 new human secreted polypeptides useful for
CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
CC conditions, respiratory disorders, cancers, CNS disorders, or
CC neurodegenerative disorders, or polypeptides comprising an amino acid
CC sequence at least 95% identical to the new sequences. The polypeptides,
CC antibodies or antibody fragments that bind to the polypeptides, nucleic
CC acids encoding the polypeptides, agonists or antagonists that binds to
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
CC compositions for diagnosing, treating or preventing an e.g. immune
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
CC polynucleotides are useful for chromosome identification, chromosome
CC mapping, for controlling gene expression through triple helix formation
CC or antisense DNA or RNA, in gene therapy, for identifying individuals
CC from minute biological samples, in forensic biology, and as hybridization
CC probes. The polypeptides are useful for as molecular weight markers on
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC gels, to raise antibodies, for testing biological activities, and for
CC treating or preventing neural disorders, immune system disorders,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, proliferative and/or cancerous diseases. This sequence corresponds
CC to a bacterial artificial chromosome (BAC) fragment containing the gene
CC encoding one of the polypeptides of the invention. Note: The sequence
CC data for this patent did form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 19521 BP; 5672 A; 3465 C; 3902 G; 6482 T; 0 U; 0 Other;

Query Match 22.2%; Score 30.8; DB 10; Length 19521;
Best Local Similarity 63.5%; Pred. No. 13;
Matches 47; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 1 GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGG 60
|| ||||||| | || || |||| | ||||||| | ||| | | ||||| ||
Db 1311 GTAACTCTGGGCAACTTACATAAACTCTCTGTGCCTCAGCTTCTGCACCTGAGAAAAGGG 1252

Qy 61 GTGACTATTTGTCT 74
| || ||| | |
Db 1251 CTAACAATTCCTAT 1238

RESULT 11
ACA02032
ID ACA02032 standard; DNA; 1539 BP.
XX
AC ACA02032;
XX
DT 04-JUN-2003 (first entry)
XX
DE C. glutamicum derived ORF SEQ ID 2023.
XX
KW Coryneform; nucleic acid array; fermentation; culture; ds.
XX
OS Corynebacterium glutamicum.
XX
PN DE10128510-A1.

```
XX
PD   19-DEC-2002.
XX
PF   13-JUN-2001; 2001DE-01028510.
XX
PR   13-JUN-2001; 2001DE-01028510.
XX
PA   (DEGS ) DEGUSSA AG.
XX
PI   Farwick M,  Moeckel B,  Pfefferle W,  Bathe B,  Huthmacher K;
XX
DR   WPI; 2003-279970/28.
XX
PT   New nucleic acid array useful for monitoring mRNA expression of
PT   Corynebacterium glutamicum during fermentation, comprising nucleic acid
PT   from Corynebacterium glutamicum.
XX
PS   Claim 1; Page 665-666; 709pp; German.
XX
CC   This invention describes a novel nucleic acid array involving
CC   Corynebacterium glutamicum polynucleotides. The arrays are used to
CC   analyse C. glutamicum, particularly for monitoring a fermentation process
CC   to determine expression levels of C. glutamicum cellular mRNA. Such
CC   monitoring particularly differentiates between expression levels of
CC   different strains of C. glutamicum and allows the adjustment of different
CC   culture and fermentation conditions. ACA00010-ACA02188 represent C.
CC   glutamicum derived polynucleotides described in the disclosure of the
CC   invention
XX
SQ   Sequence 1539 BP; 393 A; 394 C; 414 G; 338 T; 0 U; 0 Other;

  Query Match             22.0%;  Score 30.6;  DB 8;  Length 1539;
  Best Local Similarity   53.8%;  Pred. No. 7.5;
  Matches   63;  Conservative    0;  Mismatches   54;  Indels    0;  Gaps    0;

Qy         17 AACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGG 76
              ||| | | | ||| | ||     | |  ||  | |||||  |       | ||| ||  ||
Db        241 AACGTCATTGATGGCAGCGAAGGCATGCTTCATGCAGAAGAACTCAACCCATTGGTTGGG 300

Qy         77 TTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTT 133
                | ||  || || | |   || | ||||| | ||| || |  |  ||  | || | |
Db        301 ATCATCGACAGTGTCTGTTCACACCACCAAATTCACCGATCCAACGTGATGATCGGT 357


RESULT 12
AAH67957
ID   AAH67957 standard; DNA; 2799 BP.
XX
AC   AAH67957;
XX
DT   26-SEP-2001  (first entry)
XX
DE   C glutamicum coding sequence fragment SEQ ID NO: 2992.
XX
KW   Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KW   organic acid synthesis; ds.
XX
OS   Corynebacterium glutamicum.
XX
PN   EP1108790-A2.
XX
PD   20-JUN-2001.
XX
PF   18-DEC-2000; 2000EP-00127688.
XX
PR   16-DEC-1999;   99JP-00377484.
PR   07-APR-2000; 2000JP-00159162.
PR   03-AUG-2000; 2000JP-00280988.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Nakagawa S,  Mizoguchi H,  Ando S,  Hayashi M,  Ochiai K,  Yokoi H;
PI   Tateishi N,  Senoh A,  Ikeda M,  Ozaki A;
XX
DR   WPI; 2001-376931/40.
DR   P-PSDB; AAG92738.
XX
PT   Novel polynucleotides derived from Coryneform bacteria, for identifying
PT   mutation point of a gene, measuring expression of a gene, analyzing
PT   expression profile or pattern of a gene and identifying homologous gene.
XX
PS   Claim 8; SEQ ID NO 2992; 246pp + Sequence Listing; English.
XX
CC   The present invention provides a number of nucleotide and protein
CC   sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC   are useful for identifying the mutation point of a gene derived from a
CC   mutant of coryneform bacterium, measuring expression amount and analysing
CC   the expression profile or expression pattern of a gene derived from
CC   Coryneform bacterium, and identifying a homologue of a gene derived from
CC   coryneform bacterium. Coryneform bacteria are useful for producing amino
CC   acids, nucleic acids, vitamins, saccharides and organic acids,
CC   particularly L-lysine. The present sequence is a nucleic acid described
CC   in the exemplification of the invention. Note: The sequence data for this
CC   patent did not form part of the printed specification, but was obtained
CC   in electronic format directly from the European Patent Office
XX
SQ   Sequence 2799 BP; 715 A; 731 C; 728 G; 625 T; 0 U; 0 Other;

  Query Match             22.0%;  Score 30.6;  DB 5;  Length 2799;
  Best Local Similarity   53.8%;  Pred. No. 8.9;
  Matches   63;  Conservative    0;  Mismatches   54;  Indels    0;  Gaps    0;

Qy         17 AACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGG 76
              ||| | | | ||| | ||     | |  ||  | |||||  |       | ||| ||  ||
Db        271 AACGTCATTGATGGCAGCGAAGGCATGCTTCATGCAGAAGAACTCAACCCATTGGTTGGG 330

Qy         77 TTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTT 133
                | ||  || || | |   || | ||||| | ||| || |  |  ||  | || | |
Db        331 ATCATCGACAGTGTCTGTTCACACCACCAAATTCACCGATCCAACGTGATGATCGGT 387


RESULT 13
AAH68533/c
ID   AAH68533 standard; DNA; 349980 BP.
XX
AC   AAH68533;
XX
DT   26-SEP-2001  (first entry)
XX
DE   C glutamicum coding sequence fragment SEQ ID NO: 7068.
XX
KW   Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KW   organic acid synthesis; ds.
XX
OS   Corynebacterium glutamicum.
XX
PN   EP1108790-A2.
XX
PD   20-JUN-2001.
XX
PF   18-DEC-2000; 2000EP-00127688.
XX
PR   16-DEC-1999;   99JP-00377484.
PR   07-APR-2000; 2000JP-00159162.
PR   03-AUG-2000; 2000JP-00280988.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Nakagawa S,  Mizoguchi H,  Ando S,  Hayashi M,  Ochiai K,  Yokoi H;
PI   Tateishi N,  Senoh A,  Ikeda M,  Ozaki A;
XX
DR   WPI; 2001-376931/40.
XX
PT   Novel polynucleotides derived from Coryneform bacteria, for identifying
PT   mutation point of a gene, measuring expression of a gene, analyzing
PT   expression profile or pattern of a gene and identifying homologous gene.
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```
XX
PS   Disclosure; SEQ ID NO 7068; 246pp + Sequence Listing; English.
XX
CC   The present invention provides a number of nucleotide and protein
CC   sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC   are useful for identifying the mutation point of a gene derived from a
CC   mutant of coryneform bacterium, measuring expression amount and analysing
CC   the expression profile or expression pattern of a gene derived from
CC   Coryneform bacterium, and identifying a homologue of a gene derived from
CC   coryneform bacterium. Coryneform bacteria are useful for producing amino
CC   acids, nucleic acids, vitamins, saccharides and organic acids,
CC   particularly L-lysine. The present sequence is a nucleic acid described
CC   in the exemplification of the invention. Note: The sequence data for this
CC   patent did not form part of the printed specification, but was obtained
CC   in electronic format directly from the European Patent Office
XX
SQ   Sequence 349980 BP; 81250 A; 97718 C; 90621 G; 80391 T; 0 U; 0 Other;

  Query Match             22.0%;  Score 30.6;  DB 5;  Length 349980;
  Best Local Similarity   53.8%;  Pred. No. 35;
  Matches   63;  Conservative    0;  Mismatches   54;  Indels    0;  Gaps    0;

Qy         17 AACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGG 76
              ||| | | | ||| | ||     | |  ||  | |||||  |      | ||| ||  ||
Db     200056 AACGTCATTGATGGCAGCGAAGGCATGCTTCATGCAGAAGAACTCAACCCATTGGTTGGG 199997

Qy         77 TTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTT 133
                | ||  || || | |   || | ||||| | ||| || |  |  ||  | || | |
Db     199996 ATCATCGACAGTGTCTGTTCACACCACCAAATTCACCGATCCAACGTGATGATCGGT 199940


RESULT 14
AAD63515/c
ID   AAD63515 standard; DNA; 31241 BP.
XX
AC   AAD63515;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Mycoplasma genitalium gene involved in transport and binding.
XX
KW   Genetic operating system; nanomachine genome; bioreactor; bioremediation;
KW   therapeutic biomolecule; energy conversion system; processing system;
KW   anabolic; catabolic system; biological film; cosmetic application;
KW   coating; ds.
XX
OS   Mycoplasma genitalium.
XX
PN   US2003138777-A1.
XX
PD   24-JUL-2003.
XX
PF   20-SEP-2001; 2001US-00960858.
XX
PR   20-SEP-2001; 2001US-00960858.
XX
PA   (EVAN/) EVANS G A.
XX
PI   Evans GA;
XX
DR   WPI; 2003-851721/79.
XX
PT   Basic genetic operating system for an autonomous prototrophic
PT   nanomachine, comprises a nanomachine genome encoding a minimal gene set.
XX
PS   Example 1; Page 127-141; 170pp; English.
XX
CC   The invention relates to a basic genetic operating system which comprises
CC   a nanomachine genome encoding a minimal gene set for viability. The basic
CC   genetic operating system is used for an autonomous prototrophic
CC   nanomachine or autonomous auxotrophic nanomachine. The nanomachine is
CC   used as a bioreactor, for bioremediation, for production of a therapeutic
CC   biomolecule or as therapeutic agent, for production of a diagnostic
CC   indicator or as a diagnostic reagent, as a delivery system, as an
CC   artificial tissue or organ system, an energy conversion system, as a
CC   processing system, as an anabolic or catabolic system, for production of
CC   biological films or coatings that may respond to the environment and for
CC   cosmetic applications including pharmaceuticals. The present sequence is
CC   Mycoplasma genitalium nanomachine gene
XX
SQ   Sequence 31241 BP; 10733 A; 4570 C; 5361 G; 10577 T; 0 U; 0 Other;

  Query Match             21.9%;  Score 30.4;  DB 10;  Length 31241;
  Best Local Similarity   55.8%;  Pred. No. 20;
  Matches   58;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy         34 CCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATC 93
              ||||| ||  |||| || |   |   |||| | ||    |    | ||  ||  || ||
Db     25866 CCTCAGCCAATTTTTTTTAACCAAGTGGTGAGTTTTACCATCTGGTTTTGTCTTCTTGTC 25807

Qy         94 CCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTAACA 137
                 |||  | |   ||||  ||| ||   | || ||| ||| |
Db     25806 ATTAAAAGAACGCTATCAAATCTATACCCCTTTTTTTGCTAAAA 25763


RESULT 15
ACC69145/c
ID   ACC69145 standard; DNA; 31241 BP.
XX
AC   ACC69145;
XX
DT   10-JUL-2003  (first entry)
XX
DE   M. genitalium transport and binding gene cassette DNA SEQ ID NO:13.
XX
KW   Mycoplasma genitalium; gene cassette; replication; transcription;
KW   translation; metabolism; basic genetic operating system; gene therapy;
KW   autonomous prototrophic nanomachine; auxotrophic nanomachine;
KW   nanomachine; bioreactor; bioremediation; therapeutic; delivery system;
KW   artificial tissue; artificial organ system; energy conversion system;
KW   processing system; anabolic system; catabolic system; biological film;
KW   biological coating; cosmetic; gene; ds.
XX
OS   Mycoplasma genitalium.
XX
PN   WO2003025145-A2.
XX
PD   27-MAR-2003.
XX
PF   18-SEP-2002; 2002WO-US029811.
XX
PR   20-SEP-2001; 2001US-00960870.
XX
PA   (EGEA-) EGEA BIOSCIENCES INC.
XX
PI   Evans GA;
XX
DR   WPI; 2003-354602/33.
XX
PT   New basic genetic operating system for autonomous prototrophic or
PT   auxotrophic nanomachine, useful for therapeutic, diagnostic or industrial
PT   purposes, comprises a nanomachine genome encoding a gene set for
PT   viability or replication.
XX
PS   Example 1; Page 231-240; 250pp; English.
XX
CC   The present invention describes a basic genetic operating system for an
CC   autonomous prototrophic or auxotrophic nanomachine comprising a
CC   nanomachine genome encoding a minimal gene set sufficient for viability
CC   or replication, optionally in the presence of an auxotrophic molecule.
CC   Also described is an autonomous prototrophic or auxotrophic nanomachine
CC   comprising a basic genetic operating system for autonomous prototrophic
CC   or auxotrophic viability or replication, optionally in the presence of an
CC   auxotrophic molecule, and a particle envelope. The nanomachines can be
CC   used in gene therapy. The basic genetic operating system or nanomachine
CC   is useful in therapeutic, diagnostic and industrial applications, e.g. as
```

```
CC   a bioreactor, for bioremediation, for the production of a therapeutic
CC   biomolecule or as a therapeutic reagent, for the production of a
CC   diagnostic indicator or reagent, as a delivery system, as an artificial
CC   tissue or organ system, as an energy conversion system, as a processing
CC   system, as an anabolic or catabolic system, for the production of
CC   biological films or coatings, and for cosmetic applications. The present
CC   sequence represents a Mycoplasma genitalium gene cassette nucleotide
CC   sequence, which is used in an example from the present invention for the
CC   design and synthesis of a basic genetic operation system for a
CC   replication competent nanomachine
XX
SQ   Sequence 31241 BP; 10733 A; 4570 C; 5361 G; 10577 T; 0 U; 0 Other;

  Query Match             21.9%;  Score 30.4;  DB 10;  Length 31241;
  Best Local Similarity   55.8%;  Pred. No. 20;
  Matches   58;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy         34 CCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATC 93
              ||||| ||  |||| || |   |   ||||| | ||    |   | ||  ||  || ||
Db      25866 CCTCAGCCAATTTTTTTTAACCAAGTGGTGAGTTTTACCATCTGGTTTTGTCTTCTTGTC 25807

Qy         94 CCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTAACA 137
                |||  | |   |||||  ||| ||   |.|| ||| ||| |
Db      25806 ATTAAAAGAACGCTATCAAATCTATACCCCTTTTTTTGCTAAAA 25763


RESULT 16
ADN48950/c
ID   ADN48950 standard; DNA; 31241 BP.
XX
AC   ADN48950;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Mycoplasma genitalium functional gene fragment #13.
XX
KW   Prototrophic nanomachine; functional gene; ds.
XX
OS   Mycoplasma genitalium.
XX
PN   US2004063097-A1.
XX
PD   01-APR-2004.
XX
PF   20-SEP-2002; 2002US-00251668.
XX
PR   20-SEP-2002; 2002US-00251668.
XX
PA   (EVAN/) EVANS G A.
XX
PI   Evans GA;
XX
DR   WPI; 2004-346224/32.
XX
PT   Basic genetic operating system for autonomous prototrophic nanomachine,
PT   comprises nanomachine genome encoding minimal gene set sufficient for
PT   viability.
XX
PS   Example 1; SEQ ID NO 13; 170pp; English.
XX
CC   The present invention provides a basic genetic operating system for an
CC   autonomous prototrophic nanomachine comprises a nanomachine genome
CC   encoding a minimal gene set sufficient for viability. The present
CC   sequence is Mycoplasma genitalium functional gene fragment. This sequence
CC   is used in the exemplification of the invention.
XX
SQ   Sequence 31241 BP; 10733 A; 4570 C; 5361 G; 10577 T; 0 U; 0 Other;

  Query Match             21.9%;  Score 30.4;  DB 12;  Length 31241;
  Best Local Similarity   55.8%;  Pred. No. 20;
  Matches   58;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy         34 CCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATC 93
              ||||| ||  |||| || |   |   ||||| | ||    |   | ||  ||  || ||
Db      25866 CCTCAGCCAATTTTTTTTAACCAAGTGGTGAGTTTTACCATCTGGTTTTGTCTTCTTGTC 25807

Qy         94 CCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTAACA 137
                |||  | |   |||||  ||| ||   | || ||| ||| |
Db      25806 ATTAAAAGAACGCTATCAAATCTATACCCCTTTTTTTGCTAAAA 25763


RESULT 17
ABQ99653/c
ID   ABQ99653 standard; DNA; 104644 BP.
XX
AC   ABQ99653;
XX
DT   12-NOV-2002  (first entry)
XX
DE   Human MS4A7, MS4A5 and MS4A12 genomic sequence.
XX
KW   Human; membrane spanning 4-domain A; cytostatic; antiallergic; MS4A;
KW   gene therapy; atopic disorder; non-Hodgkin's lymphoma; MS4A7; MS4A12;
KW   Hodgkin's lymphoma; allergenic disease; gene; ss; chromosome 11q12-13.1;
KW   MS4A5.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             17493. .28213
FT                   /*tag=  a
FT                   /product= "MS4A7"
FT                   /note= "Contains 5 introns"
FT   exon            17493. .17639
FT                   /*tag=  b
FT                   /number= 1
FT   intron          17640. .19438
FT                   /*tag=  c
FT                   /number= 1
FT   exon            19439. .19573
FT                   /*tag=  d
FT                   /number= 2
FT   intron          19574. .21067
FT                   /*tag=  e
FT                   /number= 2
FT   exon            21068. .21124
FT                   /*tag=  f
FT                   /number= 3
FT   intron          21125. .23740
FT                   /*tag=  g
FT                   /number= 3
FT   exon            23741. .23947
FT                   /*tag=  h
FT                   /number= 4
FT   intron          23948. .27036
FT                   /*tag=  i
FT                   /number= 4
FT   exon            27037. .27138
FT                   /*tag=  j
FT                   /number= 5
FT   intron          27139. .28138
FT                   /*tag=  k
FT                   /number= 5
FT   exon            28139. .28210
FT                   /*tag=  l
FT                   /number= 6
FT   CDS             64028. .82112
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FT                   /product= "MS4A5"
FT                   /note= "Contains 4 introns"
FT   exon            64028. .64180
FT                   /*tag=  n
FT                   /number= 1
FT   intron          64181. .65148
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FT                   /number= 1
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FT                   /cons_splice= (5'site:YES,3'site:NO)
FT   exon            65149. .65277
FT                   /*tag= p
FT                   /number= 2
FT   intron          65278. .66763
FT                   /*tag= q
FT                   /number= 2
FT   exon            66764. .66820
FT                   /*tag= r
FT                   /number= 3
FT   intron          66821. .68117
FT                   /*tag= s
FT                   /number= 3
FT   exon            68118. .68270
FT                   /*tag= t
FT                   /number= 4
FT   intron          68271. .82001
FT                   /*tag= u
FT                   /number= 4
FT   exon            82002. .82109
FT                   /*tag= v
FT                   /number= 5
FT   CDS             91488. .101286
FT                   /*tag= x
FT                   /product= "MS4A12"
FT                   /note= "Contains 5 introns"
FT   exon            91488. .91760
FT                   /*tag= y
FT                   /number= 1
FT   intron          91761. .95209
FT                   /*tag= z
FT                   /number= 1
FT   exon            95210. .95347
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FT                   /number= 2
FT   intron          95348. .96147
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FT                   /number= 2
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FT                   /number= 3
FT   intron          96205. .97864
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FT                   /number= 3
FT   exon            97865. .97981
FT                   /*tag= ae
FT                   /number= 4
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FT                   /*tag= af
FT                   /number= 4
FT                   /cons_splice= (5'site:YES,3'site:NO)
FT   exon            100890. .101000
FT                   /*tag= ag
FT                   /number= 5
FT   intron          101001. .101181
FT                   /*tag= ah
FT                   /number= 5
FT   exon            101182. .101283
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FT                   /number= 6
XX
PN   WO200262946-A2.
XX
PD   15-AUG-2002.
XX
PF   10-DEC-2001; 2001WO-US048437.
XX
PR   08-DEC-2000; 2000US-0254362P.
PR   20-FEB-2001; 2001US-0270057P.
XX
PA   (UYDU-) UNIV DUKE.
XX
PI   Tedder TF, Liang YH;
XX
DR   WPI; 2002-657530/70.
DR   P-PSDB; ABP65025, ABP65029, ABP65045.
XX
PT   New membrane spanning 4-domain A (MS4A) genes and polypeptides, useful
PT   for generating animal models of atopic disorders, for drug screening, or
PT   for treating (non-) Hodgkin's lymphoma, or allergenic or atopic disorders
PT   in e.g. humans.
XX
PS   Claim 18; Page 328-385; 450pp; English.
XX
CC   The invention relates to novel membrane spanning 4-domain A (MS4A)
CC   nucleic acid and polypeptide molecules, comprising human and mouse MS4A.
CC   The polypeptides of the invention have cytostatic and antiallergic
CC   activity. The polynucleotides may have a use in gene therapy. The MS4A
CC   nucleic acids and polypeptides are useful for generating animal (e.g.
CC   mouse) models of atopic disorders, or for drug discovery screens. These
CC   are also useful for treating (non-)Hodgkin's lymphoma, allergenic
CC   diseases, atopic disorders or other MS4A-related conditions. The present
CC   sequence represents a human MS4A genomic region, encoding the MS4A7,
CC   MS4A5 and MS4A12 proteins
XX
SQ   Sequence 104644 BP; 33140 A; 20880 C; 20558 G; 29988 T; 0 U; 78 Other;

  Query Match             21.9%;  Score 30.4;  DB 6;  Length 104644;
  Best Local Similarity   53.3%;  Pred. No. 29;
  Matches   64;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy         16 GAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTG 75
              ||||  | || || | || ||    || |  |  | || |     |   ||  |||  |||
Db      88420 GAACCCAGATTATTCATGGCTAGGTCTATAGTTATTAGGACTCAGAATACATTTTTACTG 88361

Qy         76 GTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTAA 135
                | | |    ||| || |    || | |  | |  ||  || || | ||||| ||| || |
Db      88360 GGTCAAGTTCTGGTTTTATAAAAGGAATTAAAGACAGAGCCAGCCAGTTCTGATTCTTTA 88301


RESULT 18
ADB12064_03/c
Continuation (4 of 18) of ADB12064 from base 300001 (Alloiococcus otitis entire genome se
WP Sequence split into 18 fragments  LOCUS ADB12064 Accession Adb12064
WP     Fragment Name      Begin      End
WP     ADB12064_00            1    110000
WP     ADB12064_01       100001    210000
WP     ADB12064_02       200001    310000
WP     ADB12064_03       300001    410000
WP     ADB12064_04       400001    510000
WP     ADB12064_05       500001    610000
WP     ADB12064_06       600001    710000
WP     ADB12064_07       700001    810000
WP     ADB12064_08       800001    910000
WP     ADB12064_09       900001   1010000
WP     ADB12064_10      1000001   1110000
WP     ADB12064_11      1100001   1210000
WP     ADB12064_12      1200001   1310000
WP     ADB12064_13      1300001   1410000
WP     ADB12064_14      1400001   1510000
WP     ADB12064_15      1500001   1610000
WP     ADB12064_16      1600001   1710000
WP     ADB12064_17      1700001   1754382

  Query Match             21.7%;  Score 30.2;  DB 9;  Length 110000;
  Best Local Similarity   51.1%;  Pred. No. 34;
  Matches   71;  Conservative    0;  Mismatches   68;  Indels    0;  Gaps    0;

Qy          1 GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGG 60
              || | | |  ||||  |||||| | || |  |  | | | ||| || |||  |||  |
Db      57300 GTAATTTTTCTCGAACAACTTAAGTTATTCGAGAATGATCATCTATTTTTCTCAAACTGA 57241

Qy         61 GTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGAC 120
                  | || |    ||   ||  | |  ||  |     ||  ||   ||| ||| |
Db      57240 ACACTAAATTTTAAAATTACATATGTTTCGATTGCTTCCCCATTATTCCCAAAACTACAA 57181
```

```
Qy        121 TGTTCTTATTGTTAACACA 139
                || | |||| | |||
Db      57180 CCAGCTAACTGTTTAAACA 57162


RESULT 19
ADJ38283
ID   ADJ38283 standard; cDNA; 622 BP.
XX
AC   ADJ38283;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Plastid division-related Arc6 orthlogue cDNA 64.
XX
KW   prokaryotic type; plastid division; Ftn2; ARC6; ARC5; Fzo; plant cell;
KW   agronomic; horticultural; crop plant; ornamental plant; woody plant;
KW   herbicide target; gene; ss.
XX
OS   Prunus persica.
XX
PN   WO2004001003-A2.
XX
PD   31-DEC-2003.
XX
PF   20-JUN-2003; 2003WO-US019536.
XX
PR   20-JUN-2002; 2002US-0390140P.
PR   09-AUG-2002; 2002US-0402242P.
PR   20-JUN-2003; 2003US-00600070.
XX
PA   (UNMS ) UNIV MICHIGAN STATE.
XX
PI   Osteryoung KW,  Vitha S,  Koksharova OA,  Gao H;
XX
DR   WPI; 2004-082486/08.
XX
PT   New isolated Ftn2, ARC5 and/or Fzo-like nucleic acid sequences, useful
PT   for further characterizing plastid division in plant cells, and in
PT   varying agronomic and horticultural characteristics of economically
PT   important plants.
XX
PS   Disclosure; Fig 26; 287pp; English.
XX
CC   This invention relates to novel prokaryotic type or plastid division and
CC   related genes and proteins. In particular, the invention relates to novel
CC   Ftn2 (ARC6), ARC5 and Fzo-like genes and polypeptides. The methods and
CC   compositions of the present invention are useful for further
CC   characterising plastid division in plant cells, in order to vary
CC   agronomic and horticultural characteristics of economically important
CC   plants, such as crop, ornamental and woody plants. They can also be used
CC   as herbicide targets. The present sequence is a cDNA sequence which is
CC   related to the invention.
XX
SQ   Sequence 622 BP; 168 A; 125 C; 147 G; 181 T; 0 U; 1 Other;

  Query Match             21.6%;  Score 30;  DB 12;  Length 622;
  Best Local Similarity   72.2%;  Pred. No. 9.1;
  Matches   39;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy         23 AATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGG 76
              | || | |||   |||  || | ||||||||||||| ||||| |||||   |||
Db        262 ATTACTTCCTATATCAGTCTATCTTCTTCAGAAAGATGGTGAGTATTTAAGTGG 315


RESULT 20
AAK74790/c
ID   AAK74790 standard; DNA; 10711 BP.
XX
AC   AAK74790;
XX
DT   07-NOV-2001  (first entry)
XX
DE   Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29602.
XX
KW   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW   cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS   Homo sapiens.
XX
PN   WO200157182-A2.
XX
PD   09-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001354.
XX
PR   31-JAN-2000; 2000US-0179065P.
PR   04-FEB-2000; 2000US-0180628P.
PR   24-FEB-2000; 2000US-0184664P.
PR   02-MAR-2000; 2000US-0186350P.
PR   16-MAR-2000; 2000US-0189874P.
PR   17-MAR-2000; 2000US-0190076P.
PR   18-APR-2000; 2000US-0198123P.
PR   19-MAY-2000; 2000US-0205515P.
PR   07-JUN-2000; 2000US-0209467P.
PR   28-JUN-2000; 2000US-0214886P.
PR   30-JUN-2000; 2000US-0215135P.
PR   07-JUL-2000; 2000US-0216647P.
PR   07-JUL-2000; 2000US-0216880P.
PR   11-JUL-2000; 2000US-0217487P.
PR   11-JUL-2000; 2000US-0217496P.
PR   14-JUL-2000; 2000US-0218290P.
PR   26-JUL-2000; 2000US-0220963P.
PR   26-JUL-2000; 2000US-0220964P.
PR   14-AUG-2000; 2000US-0224518P.
PR   14-AUG-2000; 2000US-0224519P.
PR   14-AUG-2000; 2000US-0225213P.
PR   14-AUG-2000; 2000US-0225214P.
PR   14-AUG-2000; 2000US-0225266P.
PR   14-AUG-2000; 2000US-0225267P.
PR   14-AUG-2000; 2000US-0225268P.
PR   14-AUG-2000; 2000US-0225270P.
PR   14-AUG-2000; 2000US-0225447P.
PR   14-AUG-2000; 2000US-0225757P.
PR   14-AUG-2000; 2000US-0225758P.
PR   14-AUG-2000; 2000US-0225759P.
PR   18-AUG-2000; 2000US-0226279P.
PR   22-AUG-2000; 2000US-0226681P.
PR   22-AUG-2000; 2000US-0226868P.
PR   22-AUG-2000; 2000US-0227182P.
PR   23-AUG-2000; 2000US-0227009P.
PR   30-AUG-2000; 2000US-0228924P.
PR   01-SEP-2000; 2000US-0229287P.
PR   01-SEP-2000; 2000US-0229343P.
PR   01-SEP-2000; 2000US-0229344P.
PR   01-SEP-2000; 2000US-0229345P.
PR   05-SEP-2000; 2000US-0229509P.
PR   05-SEP-2000; 2000US-0229513P.
PR   06-SEP-2000; 2000US-0230437P.
PR   06-SEP-2000; 2000US-0230438P.
PR   08-SEP-2000; 2000US-0231242P.
PR   08-SEP-2000; 2000US-0231243P.
PR   08-SEP-2000; 2000US-0231244P.
PR   08-SEP-2000; 2000US-0231413P.
PR   08-SEP-2000; 2000US-0231414P.
PR   08-SEP-2000; 2000US-0232080P.
PR   08-SEP-2000; 2000US-0232081P.
PR   12-SEP-2000; 2000US-0231968P.
PR   14-SEP-2000; 2000US-0232397P.
PR   14-SEP-2000; 2000US-0232398P.
PR   14-SEP-2000; 2000US-0232399P.
PR   14-SEP-2000; 2000US-0232400P.
PR   14-SEP-2000; 2000US-0232401P.
PR   14-SEP-2000; 2000US-0233063P.
PR   14-SEP-2000; 2000US-0233064P.
PR   14-SEP-2000; 2000US-0233065P.
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PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-483426/52.
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
PS Disclosure; SEQ ID NO 29602; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 10711 BP; 3044 A; 2557 C; 2437 G; 2673 T; 0 U; 0 Other;

Query Match 21.6%; Score 30; DB 4; Length 10711;
Best Local Similarity 54.5%; Pred. No. 20;
Matches 60; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

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Qy          1 GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGG 60
              | |||| ||| | |   ||||||    |   |||||||   || ||   |   |||  ||
Db       9470 GAGACTTTGGGCAAATCACTTAATCTGTCTGTGCCTCAGTTTCCTTATCTATAAAATGGG 9411

Qy         61 GTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATC 110
              | || || | || |    | || ||| | ||       ||  |  ||| ||
Db       9410 GAGAATAATGGTGTCAACTTTTTACTTTATAAAGATTAAATAAGATAGTC 9361
```

RESULT 21
AAA06526
ID AAA06526 standard; cDNA; 301 BP.
XX
AC AAA06526;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:293.
XX
KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW immunogenic; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200004149-A2.
XX
PD 27-JAN-2000.
XX
PF 14-JUL-1999; 99WO-US015838.
XX
PR 14-JUL-1998; 98US-00115453.
PR 14-JUL-1998; 98US-00116134.
PR 23-SEP-1998; 98US-00159812.
PR 23-SEP-1998; 98US-00159822.

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PR   15-JAN-1999;   99US-00232149.
PR   15-JAN-1999;   99US-00232880.
PR   09-APR-1999;   99US-00288946.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Dillon DC,  Harlocker SL,  Yuqiu J,  Xu J,  Mitcham JL;
XX
DR   WPI; 2000-171268/15.
XX
PT   New polypeptide useful for treating and diagnosing prostate cancer
PT   comprises an immunogenic portion of prostate tumor protein.
XX
PS   Claim 1; Page 194; 263pp; English.
XX
CC   The present invention describes isolated polypeptides, comprising an
CC   immunogenic portion of a prostate tumour protein (PTP). The polypeptides
CC   and polynucleotides encoding them have cytostatic activity and can be
CC   used in vaccines and in gene therapy. The polypeptides and
CC   polynucleotides encoding them, antigen presenting cells which express the
CC   polypeptides, antibodies against the polypeptides and vaccines comprising
CC   them can be used for inhibiting the development of prostate cancer in a
CC   patient. The polypeptides can be used to generate antibodies or anti-
CC   idiotypic antibodies for passive immuno therapy. A portion of the
CC   polynucleotides encoding the polypeptides can be used as a probe or to
CC   modulate the expression of the polypeptides. AAA06241 to AAA06691 and
CC   AAY82000 to AAY82020 represent sequences used in the exemplification of
CC   the present invention
XX
SQ   Sequence 301 BP; 83 A; 73 C; 60 G; 85 T; 0 U; 0 Other;

  Query Match             21.4%;  Score 29.8;  DB 3;  Length 301;
  Best Local Similarity   56.7%;  Pred. No. 8.6;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
              || ||||      || ||  || ||| |  ||| || || | |||  | || |  | |
Db         30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
              ||||||  |    |  |  || | ||||||||||
Db         90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126


RESULT 22
AAH93642
ID   AAH93642 standard; cDNA; 301 BP.
XX
AC   AAH93642;
XX
DT   04-OCT-2001  (first entry)
XX
DE   Human prostate-specific cDNA sequence P8D8.
XX
KW   Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW   cytostatic; gene therapy; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200151633-A2.
XX
PD   19-JUL-2001.
XX
PF   16-JAN-2001; 2001WO-US001574.
XX
PR   14-JAN-2000; 2000US-00483672.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Xu J,  Dillon DC,  Mitcham JL,  Harlocker SL,  Jiang Y,  Reed SG;
PI   Kalos MD,  Panger GR,  Day CH,  Retter MW,  Stolk JA,  Skeiky YAW;
PI   Wang A,  Meagher MJ;
XX
DR   WPI; 2001-425873/45.
XX
PT   New polynucleotide encoding a prostate-specific protein, for diagnosing,
PT   monitoring and treating prostate cancer in a patient and for use in
PT   vaccines.
XX
PS   Claim 1; Page 320; 543pp; English.
XX
CC   The present invention describes polynucleotide sequences (I) which encode
CC   prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC   and can be used in vaccine production and gene therapy. (I), (II),
CC   antibodies to (II), fusion proteins comprising (II), and isolated T cells
CC   prepared using (I) or (II) are used treat cancer in a patient. (I) and
CC   the antibodies are also used in the detection of cancer in a patient. The
CC   cancer that is diagnosed or treated is particularly prostate cancer. (I)
CC   and (II) can be used in vaccines. The antibodies or (I) can be used for
CC   monitoring the progression of cancer in a patient. (I) and (II) can also
CC   be used to improve diagnostic and therapeutic methods for prostate
CC   cancer. They can indicate the level of metastasis as well as the prostate
CC   volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent
CC   polynucleotide and amino acid sequences used in the exemplification of
CC   the present invention
XX
SQ   Sequence 301 BP; 83 A; 73 C; 60 G; 85 T; 0 U; 0 Other;

  Query Match             21.4%;  Score 29.8;  DB 4;  Length 301;
  Best Local Similarity   56.7%;  Pred. No. 8.6;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
              || ||||      || ||  || ||| |  ||| || || | |||  | || |  | |
Db         30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
              ||||||  |    |  |  || | ||||||||||
Db         90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126


RESULT 23
AAS63734
ID   AAS63734 standard; cDNA; 301 BP.
XX
AC   AAS63734;
XX
DT   29-JAN-2002  (first entry)
XX
DE   Human prostate cDNA sequence #286.
XX
KW   Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX
OS   Homo sapiens.
XX
PN   WO200173032-A2.
XX
PD   04-OCT-2001.
XX
PF   27-MAR-2001; 2001WO-US009919.
XX
PR   27-MAR-2000; 2000US-00536857.
PR   09-MAY-2000; 2000US-00568100.
PR   12-MAY-2000; 2000US-00570737.
PR   13-JUN-2000; 2000US-00593793.
PR   27-JUN-2000; 2000US-00605783.
PR   09-AUG-2000; 2000US-00636215.
PR   29-AUG-2000; 2000US-00651236.
PR   06-SEP-2000; 2000US-00657279.
PR   02-OCT-2000; 2000US-00679426.
PR   10-OCT-2000; 2000US-00685166.
PR   09-NOV-2000; 2000US-00709729.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Xu J,  Dillon DC,  Mitcham JL,  Harlocker SL,  Jiang Y,  Kalos MD;
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PI   Fanger GR,  Retter MW,  Stolk JA,  Day CH,  Vedvick TS,  Carter D;
PI   Li SX,  Wang A,  Skeiky YAW,  Hepler WT,  Henderson RA;
XX
DR   WPI; 2001-639232/73.
XX
PT   New human prostate-specific polypeptides and polynucleotides useful for
PT   the diagnosis and treatment of cancer, especially prostate cancer.
XX
PS   Claim 1; Page 322; 579pp; English.
XX
CC   The invention relates to isolated prostate-specific polynucleotides,
CC   polypeptides, fusion proteins of the polypeptides, antibodies raised
CC   against the polypeptides (or antigenic epitopes derived from them) and
CC   antigen-presenting cells expressing the polypeptides. The antibodies are
CC   useful for detecting the presence of cancer, especially prostate cancer.
CC   The polypeptides, polynucleotides and the antigen-presenting cells are
CC   useful for stimulating and/or expanding T cells specific for a tumour
CC   protein, and for inhibiting the development of cancer especially prostate
CC   cancer. Compositions comprising the polynucleotide and/or polypeptide are
CC   useful for stimulating an immune response, and for treating cancer. The
CC   oligonucleotide is useful for detecting cancer. The present sequence is a
CC   prostate specific polynucleotide of the invention
XX
SQ   Sequence 301 BP; 83 A; 73 C; 60 G; 85 T; 0 U; 0 Other;

  Query Match           21.4%;  Score 29.8;  DB 4;  Length 301;
  Best Local Similarity   56.7%;  Pred. No. 8.6;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
              || ||||     || ||  || ||| |  ||| || || | |||  | || |  | |
Db         30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
              ||||||  |    |  |  || | ||||||||||
Db         90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126


RESULT 24
AAH02707
ID   AAH02707 standard; cDNA; 301 BP.
XX
AC   AAH02707;
XX
DT   14-JUN-2001  (first entry)
XX
DE   Prostate tumour antigen determined cDNA sequence for P8D8.
XX
KW   Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
KW   prostate cancer; immunogenic; cytostatic; vaccine; ss.
XX
OS   Homo sapiens.
XX
PN   WO200125272-A2.
XX
PD   12-APR-2001.
XX
PF   04-OCT-2000; 2000WO-US027464.
XX
PR   04-OCT-1999;   99US-0157455P.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Xu J,  Skeiky YAW,  Reed SG,  Cheever MA;
XX
DR   WPI; 2001-245062/25.
XX
PT   Prostate specific protein and its encoding polynucleotide, useful for the
PT   treatment and diagnosis of prostate cancer.
XX
PS   Claim 4; Page 206-207; 276pp; English.
XX
CC   The present invention describes an isolated polypeptide (I) comprising at
CC   least an immunogenic portion of a prostate tumour antigen protein or its
CC   variant. (I) have cytostatic activity and can be used in vaccine
CC   production. (I), prostate tumour antigen polynucleotides, an antigen
CC   presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
CC   pharmaceutical composition containing (I) are useful for inhibiting the
CC   development of cancer in a patient. Antibodies specific for prostate
CC   specific proteins and oligonucleotides that hybridise to a polynucleotide
CC   that encodes a prostate specific protein are useful for detecting the
CC   presence or absence of a cancer or monitoring the progression the
CC   progression of a cancer, especially prostate cancer. AAH02422 to AAH2872,
CC   AAB74798 to AAB74821 and AAB74830 are sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 301 BP; 83 A; 73 C; 60 G; 85 T; 0 U; 0 Other;

  Query Match           21.4%;  Score 29.8;  DB 4;  Length 301;
  Best Local Similarity   56.7%;  Pred. No. 8.6;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
              || ||||     || ||  || ||| |  ||| || || | |||  | || |  | |
Db         30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
              ||||||  |    |  |  || | ||||||||||
Db         90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126


RESULT 25
AAH84956
ID   AAH84956 standard; cDNA; 301 BP.
XX
AC   AAH84956;
XX
DT   25-SEP-2001  (first entry)
XX
DE   Human prostate-specific cDNA sequence JP8D8.
XX
KW   Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
KW   chromosome 22q11.2; prostate-specific protein; chromosome 1;
KW   prostate specific antigen; PSA; ss.
XX
OS   Homo sapiens.
XX
PN   WO200134802-A2.
XX
PD   17-MAY-2001.
XX
PF   09-NOV-2000; 2000WO-US030904.
XX
PR   12-NOV-1999;   99US-00439313.
PR   18-NOV-1999;   99US-00443686.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Xu J,  Dillon DC,  Mitcham JL,  Harlocker SL,  Jiang Y,  Reed SG;
PI   Kalos MD,  Retter MW,  Stolk JA,  Day CH,  Skeiky YAW,  Wang A;
XX
DR   WPI; 2001-308785/32.
XX
PT   Isolated polypeptide comprising at least an immunogenic portion of a
PT   prostate-specific protein, useful in the diagnosis and therapy of
PT   prostate cancer.
XX
PS   Claim 5; Page 220; 325pp; English.
XX
CC   The present invention describes an isolated polypeptide (P1) comprising
CC   at least an immunogenic portion of a prostate-specific protein, or its
CC   variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
CC   (N1) have cytostatic activity and can be used in vaccine production. The
CC   polypeptides, nucleic acids and antibodies from the present invention are
CC   useful in the diagnosis and therapy of prostate cancer. Prostate specific
CC   genes P704P, P712P, P774P, P775P and B305D are located in a genomic
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CC   region on chromosome 22q11.2 known as the Cat Eye Syndrome region.
CC   Prostate specific antigen (PSA) P501S was located on chromosome 1.
CC   AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide
CC   and polypeptide sequences used in the exemplification of the present
CC   invention
XX
SQ   Sequence 301 BP; 83 A; 73 C; 60 G; 85 T; 0 U; 0 Other;

  Query Match            21.4%;  Score 29.8;  DB 4;  Length 301;
  Best Local Similarity   56.7%;  Pred. No. 8.6;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
              || ||||     || ||  || ||| |  ||| || || | |||  | || |  | |
Db         30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
                ||||| |    |  |  || | ||||||||||
Db         90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126


RESULT 26
ACA59543
ID   ACA59543 standard; cDNA; 301 BP.
XX
AC   ACA59543;
XX
DT   10-JUN-2003  (first entry)
XX
DE   Prostate cancer therapy associated cDNA #286.
XX
KW   Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
KW   immunogen; cancer; prostate specific antigen; PSA;
KW   prostatic acid phosphatase; PAP; prostate specific membrane antigen;
KW   PSMA; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US2002192763-A1.
XX
PD   19-DEC-2002.
XX
PF   29-JUN-2001; 2001US-00895793.
XX
PR   04-OCT-1999;   99US-0157455P.
PR   04-OCT-2000; 2000US-00679272.
PR   28-MAR-2001; 2001US-00822827.
XX
PA   (XUJJ/) XU J.
PA   (DILL/) DILLON D C.
PA   (MITC/) MITCHAM J L.
PA   (HARL/) HARLOCKER S L.
PA   (JIAN/) JIANG Y.
PA   (KALO/) KALOS M D.
PA   (FANG/) FANGER G R.
PA   (RETT/) RETTER M W.
PA   (STOL/) STOLK J A.
PA   (DAYC/) DAY C H.
PA   (VEDV/) VEDVICK T S.
PA   (CART/) CARTER D.
PA   (LISX/) LI S X.
PA   (WANG/) WANG A.
PA   (SKEI/) SKEIKY Y A W.
PA   (HEPL/) HEPLER W T.
PA   (HEND/) HENDERSON R A.
PA   (HURA/) HURAL J.
PA   (MCNE/) MCNEILL P D.
PA   (HOUG/) HOUGHTON R L.
PA   (DBAS/) Y DE BASSOLS C V.
PA   (FOYT/) FOY T M.
XX
PI   Xu J,  Dillon DC,  Mitcham JL,  Harlocker SL,  Jiang Y,  Kalos MD;
PI   Fanger GR,  Retter MW,  Stolk JA,  Day CH,  Vedvick TS,  Carter D;
PI   Li SX,  Wang A,  Skeiky YAW,  Hepler WT,  Henderson RA,  Hural J;
PI   Mcneill PD,  Houghton RL,  Y De BassolsCV,  Foy TM;
XX
DR   WPI; 2001-245062/25.
XX
PT   Prostate specific protein and its encoding polynucleotide, useful for the
PT   treatment and diagnosis of prostate cancer.
XX
PS   Example 5; SEQ ID NO 293; 85pp; English.
XX
CC   The invention describes a fusion protein comprising at least one amino
CC   acid sequence of immunogenic portions of any of the 3 sequences not
CC   defined in the specification, or sequences having at least 70 or 90 %
CC   sequence identity to any one of the 35 sequences defined in the USPTO web
CC   site, which is encoded by any of the 4 nucleotide sequences not defined
CC   in the specification. The fusion protein, composition and methods are
CC   useful for diagnosing, preventing and/or treating cancer, particularly
CC   prostate cancer. The proteins are useful as markers to indicate the
CC   presence or absence of cancer. This sequence represents a prostate cancer
CC   therapy associated cDNA. Note: The sequence data for this patent did not
CC   form part of the printed specification, but was obtained in electronic
CC   format directly from the US patent office at
CC   seqdata.uspto.gov/sequence.html?DocID=US20020192763
XX
SQ   Sequence 301 BP; 83 A; 73 C; 60 G; 85 T; 0 U; 0 Other;

  Query Match            21.4%;  Score 29.8;  DB 5;  Length 301;
  Best Local Similarity   56.7%;  Pred. No. 8.6;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
              || ||||     || ||  || ||| |  ||| || || | |||  | || |  | |
Db         30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
                ||||| |    |  |  || | ||||||||||
Db         90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126


RESULT 27
ABL95106
ID   ABL95106 standard; cDNA; 301 BP.
XX
AC   ABL95106;
XX
DT   19-JUL-2002  (first entry)
XX
DE   Human P8D8 cDNA sequence SEQ ID NO 293.
XX
KW   Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW   gene therapy; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US2002022248-A1.
XX
PD   21-FEB-2002.
XX
PF   12-JAN-2001; 2001US-00759143.
XX
PR   25-FEB-1997;   97US-00806099.
PR   01-AUG-1997;   97US-00904804.
PR   10-FEB-1998;   98US-00020956.
PR   25-FEB-1998;   98US-00030607.
PR   14-JUL-1998;   98US-00115453.
PR   23-SEP-1998;   98US-00159812.
PR   15-JAN-1999;   99US-00232149.
PR   09-APR-1999;   99US-00288946.
PR   13-JUL-1999;   99US-00352616.
PR   12-NOV-1999;   99US-00439313.
PR   18-NOV-1999;   99US-00443686.
PR   14-JAN-2000; 2000US-00483672.
PR   27-MAR-2000; 2000US-00536857.
```

PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 10-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
XX
PA (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
DR WPI; 2002-255649/30.
XX
PT New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer.
XX
PS Claim 1; SEQ ID NO 293; 87pp; English.
XX
CC The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention
XX
SQ Sequence 301 BP; 83 A; 73 C; 60 G; 85 T; 0 U; 0 Other;

Query Match 21.4%; Score 29.8; DB 6; Length 301;
Best Local Similarity 56.7%; Pred. No. 8.6;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
|| |||| || || || ||| | ||| || || | | ||| | || | | |
Db 30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy 103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
|||||| | | | || | ||||||||||
Db 90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126

RESULT 28
ACC95270
ID ACC95270 standard; cDNA; 301 BP.
XX
AC ACC95270;
XX
DT 28-AUG-2003 (first entry)
XX
DE Prostate tumour specific cDNA sequence SEQ ID 293.
XX
KW Cytostatic; gene therapy; prostate-specific protein; PSP; human;
KW immune response; prostate cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200289747-A2.
XX
PD 14-NOV-2002.
XX
PF 09-MAY-2002; 2002WO-US014753.
XX
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
PI Mcneill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y;
PI Deng T;
XX
DR WPI; 2003-167130/16.
XX
PT New prostate-specific proteins and genes, useful in gene therapy,
PT particularly for stimulating an immune response in a patient, or treating
PT prostate cancer in a patient, as well as for diagnosing prostate cancer
PT in a patient.
XX
PS Example 5; Page 388; 691pp; English.
XX
CC The present invention relates to novel prostate-specific proteins (PSP)
CC and their coding sequences. The PSPs and their coding sequences are
CC useful for stimulating an immune response in a patient, or for treating
CC prostate cancer in a patient and for determining, detecting or diagnosing
CC the presence of a cancer in a patient. The present sequence was used to
CC illustrate the invention
XX
SQ Sequence 301 BP; 83 A; 73 C; 60 G; 85 T; 0 U; 0 Other;

Query Match 21.4%; Score 29.8; DB 8; Length 301;
Best Local Similarity 56.7%; Pred. No. 8.6;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
|| |||| || || || ||| | ||| || || | | ||| | || | | |
Db 30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy 103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
|||||| | | | || | ||||||||||
Db 90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126

RESULT 29
ADB13743
ID ADB13743 standard; cDNA; 301 BP.
XX
AC ADB13743;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human prostate specific cDNA JP8D8.
XX
KW Human; ss; prostate specific cDNA; cytostatic; immunostimulant;
KW gene therapy; cell therapy; vaccine; T-cell epitope;
KW class I major histocompatibility complex allele; MHC; prostate cancer;
KW tumour; antigen presenting cell.
XX
OS Homo sapiens.
XX
PN US2003185830-A1.
XX
PD 02-OCT-2003.
XX
PF 12-NOV-2002; 2002US-00294025.

```
XX
PR   25-FEB-1997;   97US-00806099.
PR   01-AUG-1997;   97US-00904804.
PR   09-FEB-1998;   98US-00020956.
PR   25-FEB-1998;   98US-00030607.
PR   14-JUL-1998;   98US-00115453.
PR   23-SEP-1998;   98US-00159812.
PR   15-JAN-1999;   99US-00232149.
PR   09-APR-1999;   99US-00288946.
PR   13-JUL-1999;   99US-00352616.
PR   12-NOV-1999;   99US-00439313.
PR   18-NOV-1999;   99US-00443686.
PR   14-JAN-2000; 2000US-00483672.
PR   27-MAR-2000; 2000US-00536857.
PR   09-MAY-2000; 2000US-00568100.
PR   12-MAY-2000; 2000US-00570737.
PR   13-JUN-2000; 2000US-00593793.
PR   27-JUN-2000; 2000US-00605783.
PR   09-AUG-2000; 2000US-00636215.
PR   29-AUG-2000; 2000US-00651236.
PR   06-SEP-2000; 2000US-00657279.
PR   02-OCT-2000; 2000US-00679426.
PR   10-OCT-2000; 2000US-00685166.
PR   09-NOV-2000; 2000US-00709729.
PR   12-JAN-2001; 2001US-00759143.
PR   09-FEB-2001; 2001US-00780669.
PR   09-MAY-2001; 2001US-00852911.
PR   29-JUN-2001; 2001US-00895814.
PR   10-DEC-2001; 2001US-00012896.
PR   09-MAY-2002; 2002US-00144678.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Xu J,  Stolk JA,  Kalos MD;
XX
DR   WPI; 2003-756193/71.
XX
PT   New isolated polypeptide for use in a vaccine for stimulating an immune
PT   response, or for treating or diagnosis cancer, preferably prostate
PT   cancer.
XX
PS   Example 5; Page; 101pp; English.
XX
CC   The invention relates to an isolated polypeptide comprising no more than
CC   11-542 amino acids of ADB13563 comprising a sequence ADB14487. The
CC   peptides comprise a fragment ADB13563 of that contain naturally processed
CC   T-cell epitopes for 3 class I major histocompatibility complex (MHC)
CC   alleles. ADB13563 is a polypeptide encoded by a human prostate specific
CC   cDNA, one of 648 disclosed as new. Also included are nucleic acids
CC   encoding the proteins and peptides, expression vectors, a host cell
CC   transformed with the vector, an isolated antibody (or antigen binding
CC   fragment) that specifically binds to the protein or peptide, detecting
CC   the presence of a cancer in a patient (comprising contacting a patient
CC   sample with a binding agent that binds to the peptides or a polypeptide
CC   appearing as ADB13558, detecting the amount of polypeptide that binds to
CC   the agent and comparing the amount of polypeptide to a predetermined cut-
CC   off value to determine the presence of cancer), a fusion protein
CC   comprising the peptides or proteins, stimulating or expanding T cells
CC   specific for a tumour protein comprising contacting T cells with the
CC   peptides or the isolated T cell population, treating prostate cancer in a
CC   patient comprising administering a composition comprising the peptides,
CC   nucleic acids, antibodies or compounds, determining the presence of a
CC   cancer in a patient and treating prostate cancer in a patient comprising
CC   incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated
CC   from a patient with the peptides or antigen presenting cells that express
CC   (the peptides so that the T cells proliferate, and administering the
CC   proliferated T cells to the patient. The peptides (or an oligonucleotide
CC   that hybridises to nucleic acid encoding them), is used to detect the
CC   presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC   antigen-presenting cells expressing the nucleic acid, are used to
CC   stimulate or expand T cells specific for a tumour protein. The peptides,
CC   nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC   presenting cells are used to stimulate an immune response or treat
CC   prostate cancer in a patient. The present sequence is one of the
CC   disclosed human prostate specific cDNAs. Note: Except where otherwise
CC   indicated, the sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030185830.
XX
SQ   Sequence 301 BP; 83 A; 73 C; 60 G; 85 T; 0 U; 0 Other;

  Query Match            21.4%;  Score 29.8;  DB 10;  Length 301;
  Best Local Similarity  56.7%;  Pred. No. 8.6;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
              || ||||     || ||  || ||| |  ||| || || | |||  | || |  | |
Db         30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
              |||||| |    |  |  || | ||||||||||
Db         90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126


RESULT 30
ADG26159
ID   ADG26159 standard; cDNA; 301 BP.
XX
AC   ADG26159;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human prostate-specific cDNA #286.
XX
KW   Human; prostate-specific polypeptide; gene; ss; prostate cancer;
KW   cytostatic.
XX
OS   Homo sapiens.
XX
PN   US2003157089-A1.
XX
PD   21-AUG-2003.
XX
PF   09-MAY-2002; 2002US-00144678.
XX
PR   25-FEB-1997;   97US-00806099.
PR   01-AUG-1997;   97US-00904804.
PR   09-FEB-1998;   98US-00020956.
PR   25-FEB-1998;   98US-00030607.
PR   14-JUL-1998;   98US-00115453.
PR   23-SEP-1998;   98US-00159812.
PR   15-JAN-1999;   99US-00232149.
PR   09-APR-1999;   99US-00288946.
PR   13-JUL-1999;   99US-00352616.
PR   12-NOV-1999;   99US-00439313.
PR   18-NOV-1999;   99US-00443686.
PR   14-JAN-2000; 2000US-00483672.
PR   27-MAR-2000; 2000US-00536857.
PR   09-MAY-2000; 2000US-00568100.
PR   12-MAY-2000; 2000US-00570737.
PR   13-JUN-2000; 2000US-00593793.
PR   27-JUN-2000; 2000US-00605783.
PR   09-AUG-2000; 2000US-00636215.
PR   29-AUG-2000; 2000US-00651236.
PR   06-SEP-2000; 2000US-00657279.
PR   02-OCT-2000; 2000US-00679426.
PR   10-OCT-2000; 2000US-00685166.
PR   09-NOV-2000; 2000US-00709729.
PR   12-JAN-2001; 2001US-00759143.
PR   09-FEB-2001; 2001US-00780669.
PR   09-MAY-2001; 2001US-00852911.
PR   29-JUN-2001; 2001US-00895814.
PR   10-DEC-2001; 2001US-00012896.
XX
PA   (CORI-) CORIXA CORP.
XX
```

PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
PI Mcneill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y;
PI Meagher MJ, Deng T;
XX
DR WPI; 2003-777973/73.
XX
PT New polynucleotides encoding prostate specific polypeptides isolated from
PT a human prostate tumor cDNA library are useful to diagnose and treat
PT cancer particularly prostate cancer.
XX
PS Example 5; SEQ ID NO 293; 99pp; English.
XX
CC The invention relates to human prostate-specific polypeptides and the
CC polynucleotides encoding them. The invention also relates to an isolated
CC antibody or its antigen-binding fragment that specifically binds a
CC polypeptide of the invention, a method of detecting cancer in a patient
CC comprising contacting a biological sample of the patient with an agent
CC that binds a prostate-specific polypeptide and comparing the amount of
CC bound polypeptide compared to a predetermined cut-off value and a fusion
CC protein comprising a prostate-specific polypeptide. The sequences of the
CC invention are used to diagnose and treat cancer, particularly prostate
CC cancer. This sequence represents cDNA encoding a human prostate-specific
CC polypeptide of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 301 BP; 83 A; 73 C; 60 G; 85 T; 0 U; 0 Other;

Query Match 21.4%; Score 29.8; DB 10; Length 301;
Best Local Similarity 56.7%; Pred. No. 8.6;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

```
Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
              || ||||     || ||  || ||| |  ||| || || | |||  | || |  | |
Db         30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
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Db         90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126
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Search completed: December 22, 2004, 02:36:23
Job time : 1042 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 22, 2004, 03:01:57 ; Search time 266 Seconds
(without alignments)
2884.949 Million cell updates/sec

Title: US-10-070-882A-2
Perfect score: 139
Sequence: 1 gtgactctggtcgacgaact.....ctgttcttattgttaacaca 139

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4093002 seqs, 2760418825 residues

Total number of hits satisfying chosen parameters: 8186004

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_NA:*
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	37.2	26.8	1385	16	US-10-282-122A-37352	Sequence 37352, A
c	2	31	22.3	772	17	US-10-363-829-150	Sequence 150, App
c	3	31	22.3	810	17	US-10-363-829-237	Sequence 237, App
	4	30.6	22.0	2799	9	US-09-738-626-2992	Sequence 2992, Ap
c	5	30.6	22.0	3309400	9	US-09-738-626-1	Sequence 1, Appli
c	6	30.4	21.9	31241	10	US-09-960-870-13	Sequence 13, Appl
c	7	30.4	21.9	31241	10	US-09-960-858-13	Sequence 13, Appl
c	8	30.4	21.9	31241	16	US-10-251-668-13	Sequence 13, Appl
c	9	30.4	21.9	104644	17	US-10-433-287-79	Sequence 79, Appl
c	10	30.4	21.9	109559	17	US-10-322-281-137	Sequence 137, App
	11	30.2	21.7	138363	17	US-10-367-094-117	Sequence 117, App
c	12	30	21.6	458	16	US-10-424-599-105245	Sequence 105245,
	13	30	21.6	622	17	US-10-600-070-201	Sequence 201, App
	14	29.8	21.4	301	9	US-09-759-143-293	Sequence 293, App
	15	29.8	21.4	301	9	US-09-780-669-293	Sequence 293, App
	16	29.8	21.4	301	9	US-09-822-827-293	Sequence 293, App
	17	29.8	21.4	301	9	US-09-232-880-293	Sequence 293, App
	18	29.8	21.4	301	9	US-09-895-793-293	Sequence 293, App
	19	29.8	21.4	301	9	US-09-895-814-293	Sequence 293, App
	20	29.8	21.4	301	13	US-10-012-896-293	Sequence 293, App
	21	29.8	21.4	301	14	US-10-010-940-293	Sequence 293, App
	22	29.8	21.4	301	15	US-10-144-678A-293	Sequence 293, App
	23	29.8	21.4	301	15	US-10-294-025-293	Sequence 293, App
	24	29.8	21.4	434	15	US-10-102-524-307	Sequence 307, App
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	26	29.8	21.4	444	13	US-10-027-632-81146	Sequence 81146, A
	27	29.8	21.4	444	15	US-10-027-632-81146	Sequence 81146, A
	28	29.8	21.4	463	13	US-10-027-632-109769	Sequence 109769,
	29	29.8	21.4	463	15	US-10-027-632-109769	Sequence 109769,
	30	29.8	21.4	492	9	US-09-954-456-46	Sequence 46, Appl
	31	29.8	21.4	492	9	US-09-954-456-962	Sequence 962, App
	32	29.8	21.4	617	13	US-10-027-632-229999	Sequence 229999,
	33	29.8	21.4	617	15	US-10-027-632-229999	Sequence 229999,
	34	29.8	21.4	1448	16	US-10-131-487A-46	Sequence 46, Appl
	35	29.8	21.4	2962	15	US-10-104-047-1343	Sequence 1343, Ap
	36	29.8	21.4	3042	15	US-10-205-823-155	Sequence 155, App
	37	29.8	21.4	3042	15	US-10-177-293-183	Sequence 183, App
	38	29.8	21.4	3042	15	US-10-210-120-114	Sequence 114, App
	39	29.8	21.4	3042	15	US-10-341-434-120	Sequence 120, App
	40	29.8	21.4	3042	15	US-10-172-118-1654	Sequence 1654, Ap
	41	29.8	21.4	3042	16	US-10-342-887-1654	Sequence 1654, Ap
	42	29.8	21.4	3154	17	US-10-115-635-360	Sequence 360, App
	43	29.8	21.4	3174	16	US-10-351-334-86	Sequence 86, Appl
	44	29.6	21.3	611	13	US-10-027-632-197263	Sequence 197263,
	45	29.6	21.3	611	15	US-10-027-632-197263	Sequence 197263,
c	46	29.6	21.3	483728	18	US-10-699-156-2	Sequence 2, Appli
	47	29.4	21.2	567	13	US-10-027-632-51360	Sequence 51360, A
	48	29.4	21.2	567	15	US-10-027-632-51360	Sequence 51360, A
	49	29.4	21.2	592	13	US-10-027-632-61820	Sequence 61820, A
	50	29.4	21.2	592	15	US-10-027-632-61820	Sequence 61820, A
c	51	29.4	21.2	32249	10	US-09-764-891-7477	Sequence 7477, Ap
c	52	29.4	21.2	43602	15	US-10-085-959-18	Sequence 18, Appl
c	53	29.2	21.0	16593	8	US-08-961-527-52	Sequence 52, Appl
c	54	29.2	21.0	16593	16	US-10-158-844-52	Sequence 52, Appl
	55	29	20.9	510	13	US-10-027-632-236290	Sequence 236290,
	56	29	20.9	510	15	US-10-027-632-236290	Sequence 236290,
	57	29	20.9	607	13	US-10-027-632-13067	Sequence 13067, A
	58	29	20.9	607	15	US-10-027-632-13067	Sequence 13067, A
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c	61	28.8	20.7	2347	10	US-09-880-573-113	Sequence 113, App
c	62	28.6	20.6	481	9	US-09-783-590-1098	Sequence 1098, Ap
c	63	28.6	20.6	485	9	US-09-864-761-4049	Sequence 4049, Ap
	64	28.6	20.6	500	13	US-10-027-632-80079	Sequence 80079, A
	65	28.6	20.6	500	13	US-10-027-632-301423	Sequence 301423,
	66	28.6	20.6	500	15	US-10-027-632-80079	Sequence 80079, A
	67	28.6	20.6	500	15	US-10-027-632-301423	Sequence 301423,
c	68	28.6	20.6	553	13	US-10-027-632-303134	Sequence 303134,
c	69	28.6	20.6	553	15	US-10-027-632-303134	Sequence 303134,
	70	28.6	20.6	573	13	US-10-027-632-67583	Sequence 67583, A
	71	28.6	20.6	573	15	US-10-027-632-67583	Sequence 67583, A
c	72	28.6	20.6	2676	9	US-09-974-592-11	Sequence 11, Appl
c	73	28.6	20.6	16397	8	US-08-781-986A-205	Sequence 205, App
c	74	28.6	20.6	16397	16	US-10-329-624-205	Sequence 205, App
c	75	28.6	20.6	84826	13	US-10-087-192-1561	Sequence 1561, Ap
c	76	28.4	20.4	585	13	US-10-027-632-180415	Sequence 180415,
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	78	28.4	20.4	615	13	US-10-027-632-236049	Sequence 236049,
	79	28.4	20.4	615	15	US-10-027-632-236049	Sequence 236049,
	80	28.4	20.4	659	13	US-10-027-632-191479	Sequence 191479,
	81	28.4	20.4	659	15	US-10-027-632-191479	Sequence 191479,
	82	28.4	20.4	1092	15	US-10-138-701-1	Sequence 1, Appli
	83	28.4	20.4	1305	13	US-10-027-632-255960	Sequence 255960,
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c	85	28.4	20.4	2407	8	US-08-781-986A-391	Sequence 391, App

c 86	28.4	20.4	2407	16	US-10-329-624-391	Sequence 391, App
87	28.4	20.4	3450	15	US-10-369-493-46078	Sequence 46078, A
88	28.4	20.4	5549	8	US-08-781-986A-188	Sequence 188, App
89	28.4	20.4	5549	16	US-10-329-624-188	Sequence 188, App
c 90	28.4	20.4	80423	17	US-10-367-094-41	Sequence 41, Appl
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93	28.2	20.3	541	16	US-10-424-599-36959	Sequence 36959, A
c 94	28.2	20.3	879	16	US-10-425-114-9454	Sequence 9454, Ap
95	28.2	20.3	1288	16	US-10-424-599-2035	Sequence 2035, Ap
96	28.2	20.3	1547	16	US-10-424-599-36958	Sequence 36958, A
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c 99	28.2	20.3	1688	15	US-10-027-632-248955	Sequence 248955,
c 100	28.2	20.3	1688	15	US-10-027-632-248956	Sequence 248956,

ALIGNMENTS

RESULT 1
US-10-282-122A-37352
; Sequence 37352, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37352
; LENGTH: 1385
; TYPE: DNA
; ORGANISM: Salmonella paratyphi A
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (72)..(72)
; OTHER INFORMATION: n=g, a, t or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (74)..(75)
; OTHER INFORMATION: n=g, a, t or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (158)..(158)
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US-10-282-122A-37352

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Best Local Similarity 92.9%; Pred. No. 0.062;
Matches 39; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 2
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; Publication No. US20040142331A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, Stuart E.; Lincoln, Stephen E.;
; APPLICANT: Altus, Christina M.; Dufour, Gerard E.;
; APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
; APPLICANT: Jones, Anissa L.; Yu, Jimmy Y.;
; APPLICANT: Wright, Rachel J.; Gietzen, Darryl;
; APPLICANT: Liu, Tommy F.; Yap, Pierre E.;
; APPLICANT: Dahl, Christopher R.; Momiyama, Monika G.;
; APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
; APPLICANT: Harris, Bernard; Roseberry Lincoln, Ann M.;
; APPLICANT: Gerstin,Jr., Edward H.; Peralta, Careyna H.;
; APPLICANT: David, Marie H.; Panzer, Scott R.;
; APPLICANT: Flores, Vincent Z.; Daffo, Abel;
; APPLICANT: Marwaha, Rakesh; Chen, Alice J.;
; APPLICANT: Chang, Simon C.; Au, Alan P.;
; APPLICANT: Inman, Rebekah R.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1183 USN
; CURRENT APPLICATION NUMBER: US/10/363,829
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: PCT/US01/27628
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/229,751
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,749
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,750
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,747
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,748
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,583
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,517
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,610
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,597
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PERL Program
; SEQ ID NO 150
; LENGTH: 772
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: LG:994938.1:2000SEP08
US-10-363-829-150

Query Match 22.3%; Score 31; DB 17; Length 772;
Best Local Similarity 57.9%; Pred. No. 5.9;
Matches 55; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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Qy        105 ATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
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RESULT 3
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; Sequence 237, Application US/10363829
; Publication No. US20040142331A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, Stuart E.; Lincoln, Stephen E.;
; APPLICANT: Altus, Christina M.; Dufour, Gerard E.;
; APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
; APPLICANT: Jones, Anissa L.; Yu, Jimmy Y.;
; APPLICANT: Wright, Rachel J.; Gietzen, Darryl;
; APPLICANT: Liu, Tommy F.; Yap, Pierre E.;
; APPLICANT: Dahl, Christopher R.; Momiyama, Monika G.;
; APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
; APPLICANT: Harris, Bernard; Roseberry Lincoln, Ann M.;
; APPLICANT: Gerstin,Jr., Edward H.; Peralta, Careyna H.;
; APPLICANT: David, Marie H.; Panzer, Scott R.;
; APPLICANT: Flores, Vincent Z.; Daffo, Abel;
; APPLICANT: Marwaha, Rakesh; Chen, Alice J.;
; APPLICANT: Chang, Simon C.; Au, Alan P.;
; APPLICANT: Inman, Rebekah R.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1183 USN
; CURRENT APPLICATION NUMBER: US/10/363,829
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: PCT/US01/27628
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/229,751
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,749
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,750
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,747
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,748
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,583
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,517
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,610
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,597
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PERL Program
; SEQ ID NO 237
; LENGTH: 810
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: LI:814261.1:2000SEP08
US-10-363-829-237

Query Match 22.3%; Score 31; DB 17; Length 810;
Best Local Similarity 57.9%; Pred. No. 6.1;
Matches 55; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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Qy        105 ATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
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RESULT 4
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; Sequence 2992, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 2992
; LENGTH: 2799
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-2992

Query Match 22.0%; Score 30.6; DB 9; Length 2799;
Best Local Similarity 53.8%; Pred. No. 14;
Matches 63; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

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Qy         77 TTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTT 133
                | ||  || || | |   || | ||||| | ||| || |  |  ||  | || | |
Db        331 ATCATCGACAGTGTCTGTTCACACCACCAAATTCACCGATCCAACGTGATGATCGGT 387
```

RESULT 5
US-09-738-626-1/c
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125

```
;  CURRENT APPLICATION NUMBER: US/09/738,626
;  CURRENT FILING DATE:  2000-12-18
;  PRIOR APPLICATION NUMBER: JP 99/377484
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: JP 00/159162
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: JP 00/280988
;  PRIOR FILING DATE: 2000-08-03
;  NUMBER OF SEQ ID NOS: 7059
;  SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
;   LENGTH: 3309400
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

  Query Match             22.0%;  Score 30.6;  DB 9;  Length 3309400;
  Best Local Similarity   53.8%;  Pred. No. 2.6e+02;
  Matches   63;  Conservative    0;  Mismatches   54;  Indels    0;  Gaps    0;

Qy         17 AACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGG 76
              ||| | | | ||| | ||      | |  ||  | |||||  |      | ||| ||  ||
Db    2900056 AACGTCATTGATGGCAGCGAAGGCATGCTTCATGCAGAAGAACTCAACCCATTGGTTGGG 2899997

Qy         77 TTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTT 133
              | ||  || || | |   || | ||||| | ||| || |  |  ||  | || | |
Db    2899996 ATCATCGACAGTGTCTGTTCACACCACCAAATTCACCGATCCAACGTGATGATCGGT 2899940


RESULT 6
US-09-960-870-13/c
; Sequence 13, Application US/09960870
; Publication No. US20030134281A1
; GENERAL INFORMATION:
;  APPLICANT: Evans, Glen
;  TITLE OF INVENTION: NANOMACHINE COMPOSITIONS AND METHODS OF
;  TITLE OF INVENTION:  USE
;  FILE REFERENCE: P-EA 4738
;  CURRENT APPLICATION NUMBER: US/09/960,870
;  CURRENT FILING DATE:  2001-09-20
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 31241
;   TYPE: DNA
;   ORGANISM: M. genitalium
US-09-960-870-13

  Query Match             21.9%;  Score 30.4;  DB 10;  Length 31241;
  Best Local Similarity   55.8%;  Pred. No. 45;
  Matches   58;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy         34 CCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATC 93
              |||||  ||  ||||  || |   |   |||||  | ||     |    | ||  ||  || ||
Db      25866 CCTCAGCCAATTTTTTTTAACCAAGTGGTGAGTTTTACCATCTGGTTTTGTCTTCTTGTC 25807

Qy         94 CCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTAACA 137
              |||  | |   |||||  ||| ||   | || ||| ||| |
Db      25806 ATTAAAAGAACGCTATCAAATCTATACCCCTTTTTTTGCTAAAA 25763


RESULT 7
US-09-960-858-13/c
; Sequence 13, Application US/09960858
; Publication No. US20030138777A1
; GENERAL INFORMATION:
;  APPLICANT: Evans, Glen
;  TITLE OF INVENTION: NANOMACHINE COMPOSITIONS AND METHODS OF
;  TITLE OF INVENTION:  USE
;  FILE REFERENCE: P-EA 4974
;  CURRENT APPLICATION NUMBER: US/09/960,858
;  CURRENT FILING DATE:  2001-09-20
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 31241
;   TYPE: DNA
;   ORGANISM: M. genitalium
US-09-960-858-13

  Query Match             21.9%;  Score 30.4;  DB 10;  Length 31241;
  Best Local Similarity   55.8%;  Pred. No. 45;
  Matches   58;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy         34 CCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATC 93
              |||||  ||  ||||  || |   |   |||||  | ||     |    | ||  ||  || ||
Db      25866 CCTCAGCCAATTTTTTTTAACCAAGTGGTGAGTTTTACCATCTGGTTTTGTCTTCTTGTC 25807

Qy         94 CCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTAACA 137
              |||  | |   |||||  ||| ||   | || ||| ||| |
Db      25806 ATTAAAAGAACGCTATCAAATCTATACCCCTTTTTTTGCTAAAA 25763


RESULT 8
US-10-251-668-13/c
; Sequence 13, Application US/10251668
; Publication No. US20040063097A1
; GENERAL INFORMATION:
;  APPLICANT: Evans, Glen
;  TITLE OF INVENTION: NANOMACHINE COMPOSITIONS AND METHODS OF
;  TITLE OF INVENTION:  USE
;  FILE REFERENCE: P-EA 5441
;  CURRENT APPLICATION NUMBER: US/10/251,668
;  CURRENT FILING DATE:  2002-09-20
;  PRIOR APPLICATION NUMBER: US 09/960,607
;  PRIOR FILING DATE: 2001-09-20
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 31241
;   TYPE: DNA
;   ORGANISM: M. genitalium
US-10-251-668-13

  Query Match             21.9%;  Score 30.4;  DB 16;  Length 31241;
  Best Local Similarity   55.8%;  Pred. No. 45;
  Matches   58;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy         34 CCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATC 93
              |||||  ||  ||||  || |   |   |||||  | ||     |    | ||  ||  || ||
Db      25866 CCTCAGCCAATTTTTTTTAACCAAGTGGTGAGTTTTACCATCTGGTTTTGTCTTCTTGTC 25807

Qy         94 CCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTAACA 137
              |||  | |   |||||  ||| ||   | || ||| ||| |
Db      25806 ATTAAAAGAACGCTATCAAATCTATACCCCTTTTTTTGCTAAAA 25763


RESULT 9
US-10-433-287-79/c
; Sequence 79, Application US/10433287
; Publication No. US20040137566A1
; GENERAL INFORMATION:
;  APPLICANT: Tedder, Thomas F
;  APPLICANT:  Liang, Yinghua
;  TITLE OF INVENTION: Identification of Novel Gene Family Members Expressed by
;  TITLE OF INVENTION:  Hematopoietic Cells
;  FILE REFERENCE: 180/132 PCT/US
;  CURRENT APPLICATION NUMBER: US/10/433,287
;  CURRENT FILING DATE:  2003-11-12
;  NUMBER OF SEQ ID NOS: 81
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79
;   LENGTH: 104644
;   TYPE: DNA
;   ORGANISM: homo sapiens
;   FEATURE:
```

```
;   NAME/KEY: genomic_DNA
;   LOCATION: (1)..(104644)
;   OTHER INFORMATION: n is an undetermined nucleotide (dATP, dCTP, dGTP, or dTTP)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(3)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (39)..(39)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (70)..(70)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (73)..(73)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (143)..(143)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (231)..(231)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (242)..(242)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (362)..(362)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (11659)..(11659)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (11699)..(11699)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: MS4A7_initial_coding_region
;   LOCATION: (17493)..(17639)
;   FEATURE:
;   NAME/KEY: MS4A7_coding_region
;   LOCATION: (19439)..(19573)
;   FEATURE:
;   NAME/KEY: MS4A7_coding_region
;   LOCATION: (21068)..(21124)
;   FEATURE:
;   NAME/KEY: MS4A7_coding_region
;   LOCATION: (23741)..(23947)
;   FEATURE:
;   NAME/KEY: MS4A7_coding_region
;   LOCATION: (27037)..(27138)
;   FEATURE:
;   NAME/KEY: MS4A7_coding_region
;   LOCATION: (28139)..(28210)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (32640)..(32640)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: MS4A5_initial_coding_region
;   LOCATION: (64028)..(64180)
;   FEATURE:
;   NAME/KEY: MS4A5_coding_region
;   LOCATION: (65149)..(65277)
;   FEATURE:
;   NAME/KEY: MS4A5_coding_region
;   LOCATION: (66764)..(66820)
;   FEATURE:
;   NAME/KEY: MS4A5_coding_region
;   LOCATION: (68118)..(68270)
;   FEATURE:
;   NAME/KEY: MS4A5_coding_region
;   LOCATION: (82002)..(82109)
;   FEATURE:
;   NAME/KEY: MS4A12_initial_coding_region
;   LOCATION: (91488)..(91760)
;   FEATURE:
;   NAME/KEY: MS4A12_coding_region
;   LOCATION: (95210)..(95347)
;   FEATURE:
;   NAME/KEY: MS4A12_coding_region
;   LOCATION: (96148)..(96204)
;   FEATURE:
;   NAME/KEY: MS4A12_coding_region
;   LOCATION: (97865)..(97981)
;   FEATURE:
;   NAME/KEY: MS4A12_coding_region
;   LOCATION: (100890)..(101000)
;   FEATURE:
;   NAME/KEY: MS4A12_coding_region
;   LOCATION: (101182)..(101283)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (104561)..(104625)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-433-287-79

  Query Match             21.9%;  Score 30.4;  DB 17;  Length 104644;
  Best Local Similarity   53.3%;  Pred. No. 75;
  Matches   64;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy         16 GAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTG 75
              ||||  | || || | || ||    || |  |  | || |    |   ||  |||  |||
Db      88420 GAACCCAGATTATTCATGGCTAGGTCTATAGTTATTAGGACTCAGAATACATTTTTACTG 88361

Qy         76 GTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTAA 135
              | | |    ||| || |    || | |  | |  ||  || || | ||||| ||| || |
Db      88360 GGTCAAGTTCTGGTTTTATAAAAGGAATTAAAGACAGAGCCAGCCAGTTCTGATTCTTTA 88301


RESULT 10
US-10-322-281-137/c
; Sequence 137, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
;  APPLICANT: David W. Morris
;  APPLICANT:  Marc S. Malandro
;  TITLE OF INVENTION: Novel Compositions and Methods in Cancer
;  FILE REFERENCE: 529452001000
;  CURRENT APPLICATION NUMBER: US/10/322,281
;  CURRENT FILING DATE:  2002-12-17
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 137
;   LENGTH: 109559
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(109559)
;   OTHER INFORMATION: n = A,T,C or G
US-10-322-281-137

  Query Match             21.9%;  Score 30.4;  DB 17;  Length 109559;
  Best Local Similarity   55.8%;  Pred. No. 77;
  Matches   58;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy          4 ACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTG 63
              | ||||| | |       |  | || || | | ||  || ||| |    ||||     |
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```
Db       8124 AATCTGGCCCAATGTTCGCAGCAGTGACTCCGTAACTATCGTTTATAAGAAAAGTCCACG 8065

Qy         64 ACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATA 107
              ||| | ||| | |   ||   |||| | || ||| |||| ||||
Db       8064 ACTTTCTGTTTTGCACATGTTCTGTGTGTCTCCACAGCAACATA 8021


RESULT 11
US-10-367-094-117
; Sequence 117, Application US/10367094
; Publication No. US20040170982A1
; GENERAL INFORMATION:
;  APPLICANT: David W. Morris
;  APPLICANT:  Marc Malandro
;  TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
;  FILE REFERENCE: 529452001500
;  CURRENT APPLICATION NUMBER: US/10/367,094
;  CURRENT FILING DATE:  2003-02-14
;  NUMBER OF SEQ ID NOS: 203
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 117
;   LENGTH: 138363
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(138363)
;   OTHER INFORMATION: n = A,T,C or G
US-10-367-094-117

  Query Match             21.7%;  Score 30.2;  DB 17;  Length 138363;
  Best Local Similarity   56.6%;  Pred. No. 99;
  Matches   56;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy         39 CCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAA 98
              | ||||||||||||   |  ||  |  ||| | | ||  |||||||| | ||| | |  ||
Db     131756 CTCTCTTTTCTTCTTTATTAGTCTAGCTAGTAGCCTATTTTATTAATTTTTTTTTCAAAA 131815

Qy         99 AGCACCATAATCAACGCTAGACTGTTCTTATTGTTAACA 137
              | |    |  | ||  |     | || | | | ||  ||
Db     131816 ATCCAGCTCCTGAATTCATTGATCTTTTGAATTTTTTCA 131854


RESULT 12
US-10-424-599-105245/c
; Sequence 105245, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 105245
;   LENGTH: 458
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(458)
;   OTHER INFORMATION: unsure at all n locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_66052C.1
US-10-424-599-105245

  Query Match             21.6%;  Score 30;  DB 16;  Length 458;
  Best Local Similarity   54.5%;  Pred. No. 10;
  Matches   60;  Conservative    0;  Mismatches   50;  Indels    0;  Gaps    0;

Qy         11 TCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTT 70
              || | |  || || | |||  ||  ||     || |||  |  |||||| |  ||
Db       193 TCTAGGGCCTCAATTTATGTATGTATCTAGTTCATTTTATGTGAAAGATGAAGAAGTCCC 134

Qy         71 GTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGAC 120
              |||  | ||||  |  | || |      |||| || |  |||||  | |||
Db       133 GTCACGATTATCATTTTTTAAATATGTAAGCTCCCTTGTCAACATTTGAC 84


RESULT 13
US-10-600-070-201
; Sequence 201, Application US/10600070
; Publication No. US20040139500A1
; GENERAL INFORMATION:
;  APPLICANT: Osteryoung, Katherine W.
;  APPLICANT:  Vitha, Stanislav
;  APPLICANT:  Koksharova, Olga A.
;  APPLICANT:  Gao, Hongo
;  TITLE OF INVENTION: Plastid Division and Related Genes and Proteins, and Methods of
;  TITLE OF INVENTION:  Use
;  FILE REFERENCE: MSU-08153
;  CURRENT APPLICATION NUMBER: US/10/600,070
;  CURRENT FILING DATE:  2003-06-20
;  NUMBER OF SEQ ID NOS: 206
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 201
;   LENGTH: 622
;   TYPE: DNA
;   ORGANISM: Prunus persica
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (609)..(609)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-600-070-201

  Query Match             21.6%;  Score 30;  DB 17;  Length 622;
  Best Local Similarity   72.2%;  Pred. No. 12;
  Matches   39;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy         23 AATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGG 76
              | || | |||   |||  || | ||||||||||||| ||||| |||||   |||
Db       262 ATTACTTCCTATATCAGTCTATCTTCTTCAGAAAGATGGTGAGTATTTAAGTGG 315


RESULT 14
US-09-759-143-293
; Sequence 293, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.427C23
;  CURRENT APPLICATION NUMBER: US/09/759,143
;  CURRENT FILING DATE:  2001-01-12
;  NUMBER OF SEQ ID NOS:  934
```

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;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 293
;   LENGTH: 301
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-759-143-293

  Query Match           21.4%;  Score 29.8;  DB 9;  Length 301;
  Best Local Similarity   56.7%;  Pred. No. 10;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
              || ||||     || ||  || ||| |  ||| || || | |||  | || |  | |
Db         30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
              |||||| |    |  |  || | ||||||||||
Db         90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126


RESULT 15
US-09-780-669-293
; Sequence 293, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  APPLICANT:  Hural, John
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Houghton, Raymond L.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.427C24
;  CURRENT APPLICATION NUMBER: US/09/780,669
;  CURRENT FILING DATE:  2001-02-09
;  NUMBER OF SEQ ID NOS:  943
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 293
;   LENGTH: 301
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-780-669-293

  Query Match           21.4%;  Score 29.8;  DB 9;  Length 301;
  Best Local Similarity   56.7%;  Pred. No. 10;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
              || ||||     || ||  || ||| |  ||| || || | |||  | || |  | |
Db         30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
              |||||| |    |  |  || | ||||||||||
Db         90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126


RESULT 16
US-09-822-827-293
; Sequence 293, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.534C1
;  CURRENT APPLICATION NUMBER: US/09/822,827
;  CURRENT FILING DATE:  2001-03-28
;  NUMBER OF SEQ ID NOS: 982
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 293
;   LENGTH: 301
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-822-827-293

  Query Match           21.4%;  Score 29.8;  DB 9;  Length 301;
  Best Local Similarity   56.7%;  Pred. No. 10;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
              || ||||     || ||  || ||| |  ||| || || | |||  | || |  | |
Db         30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
              |||||| |    |  |  || | ||||||||||
Db         90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126


RESULT 17
US-09-232-880-293
; Sequence 293, Application US/09232880
; Publication No. US20020182596A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT: Dillon, Davin C.
;  APPLICANT: Mitcham, Jennifer Lynn
;  TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
;  TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.428C6
;  CURRENT APPLICATION NUMBER: US/09/232,880
;  CURRENT FILING DATE: 1999-01-15
;  NUMBER OF SEQ ID NOS: 338
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 293
;   LENGTH: 301
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-232-880-293

  Query Match           21.4%;  Score 29.8;  DB 9;  Length 301;
  Best Local Similarity   56.7%;  Pred. No. 10;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
              || ||||     || ||  || ||| |  ||| || || | |||  | || |  | |
Db         30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
              |||||| |    |  |  || | ||||||||||
Db         90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126


RESULT 18
US-09-895-793-293
; Sequence 293, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
```

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;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel X.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Hural, John
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Vinals de Bassols, Carlota
;  APPLICANT:  Foy, Teresa
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.534C2
;  CURRENT APPLICATION NUMBER: US/09/895,793
;  CURRENT FILING DATE:  2001-06-29
;  NUMBER OF SEQ ID NOS: 982
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 293
;   LENGTH: 301
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-895-793-293

  Query Match             21.4%;  Score 29.8;  DB 9;  Length 301;
  Best Local Similarity   56.7%;  Pred. No. 10;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
              || ||||      || ||  || ||| |  ||| || || | |||  | ||| |  | |
Db         30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
              |||||| |    |  |  || | ||||||||||
Db         90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126


RESULT 19
US-09-895-814-293
; Sequence 293, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel X.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Hural, John
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Vinals de Bassols, Carlota
;  APPLICANT:  Foy, Teresa
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C26
;  CURRENT APPLICATION NUMBER: US/09/895,814
;  CURRENT FILING DATE:  2001-06-29
;  NUMBER OF SEQ ID NOS: 990
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 293
;   LENGTH: 301
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-895-814-293

  Query Match             21.4%;  Score 29.8;  DB 9;  Length 301;
  Best Local Similarity   56.7%;  Pred. No. 10;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
              || ||||      || ||  || ||| |  ||| || || | |||  | ||| |  | |
Db         30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
              |||||| |    |  |  || | ||||||||||
Db         90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126


RESULT 20
US-10-012-896-293
; Sequence 293, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel X.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Hural, John
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Vinals de Bassols, Carlota
;  APPLICANT:  Foy, Teresa
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Wantanabe, Yoshihiro
;  APPLICANT:  Meagher, Madeleine Joy
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C27
;  CURRENT APPLICATION NUMBER: US/10/012,896
;  CURRENT FILING DATE:  2001-12-10
;  NUMBER OF SEQ ID NOS: 1011
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 293
;   LENGTH: 301
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-012-896-293

  Query Match             21.4%;  Score 29.8;  DB 13;  Length 301;
  Best Local Similarity   56.7%;  Pred. No. 10;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
              || ||||      || ||  || ||| |  ||| || || | |||  | ||| |  | |
Db         30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89
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Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
              |||||| |    |  |  || | ||||||||||
Db         90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126


RESULT 21
US-10-010-940-293
; Sequence 293, Application US/10010940
; Publication No. US20030088062A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan Louise
;  APPLICANT:  Jiang Yuqui
;  APPLICANT:  Reed, Steven G.
;  APPLICANT:  Kalos, Michael
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Retter, Mark
;  APPLICANT:  Solk, John
;  APPLICANT:  Day, Craig
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427D3
;  CURRENT APPLICATION NUMBER: US/10/010,940
;  CURRENT FILING DATE:  2001-12-05
;  NUMBER OF SEQ ID NOS: 575
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 293
;   LENGTH: 301
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-010-940-293

  Query Match             21.4%;  Score 29.8;  DB 14;  Length 301;
  Best Local Similarity   56.7%;  Pred. No. 10;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
              || ||||     || ||  || ||| |  ||| || || | |||  | || |  | |
Db         30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
              |||||| |    |  |  || | ||||||||||
Db         90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126


RESULT 22
US-10-144-678A-293
; Sequence 293, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel X.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A. W.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Hural, John
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Vinals y de Bassols, Carlota
;  APPLICANT:  Foy, Teresa M.
;  APPLICANT:  Watanabe, Yoshihiro
;  APPLICANT:  Deng, Ta
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C28
;  CURRENT APPLICATION NUMBER: US/10/144,678A
;  CURRENT FILING DATE:  2002-08-12
;  NUMBER OF SEQ ID NOS: 1033
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 293
;   LENGTH: 301
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-144-678A-293

  Query Match             21.4%;  Score 29.8;  DB 15;  Length 301;
  Best Local Similarity   56.7%;  Pred. No. 10;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
              || ||||     || ||  || ||| |  ||| || || | |||  | || |  | |
Db         30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
              |||||| |    |  |  || | ||||||||||
Db         90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126


RESULT 23
US-10-294-025-293
; Sequence 293, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Kalos, Michael D.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C29
;  CURRENT APPLICATION NUMBER: US/10/294,025
;  CURRENT FILING DATE:  2002-11-12
;  NUMBER OF SEQ ID NOS: 1038
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 293
;   LENGTH: 301
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-294-025-293

  Query Match             21.4%;  Score 29.8;  DB 15;  Length 301;
  Best Local Similarity   56.7%;  Pred. No. 10;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
              || ||||     || ||  || ||| |  ||| || || | |||  | || |  | |
Db         30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
              |||||| |    |  |  || | ||||||||||
Db         90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126


RESULT 24
US-10-102-524-307
; Sequence 307, Application US/10102524
; Publication No. US20030109434A1
; GENERAL INFORMATION:
;  APPLICANT: Algate, Paul A.
;  APPLICANT:  Mannion, Jane
;  APPLICANT:  Gaiger, Alexander
;  APPLICANT:  Gordon, Brian
```

```
;  APPLICANT:  Harlocker, Susan L.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
;  TITLE OF INVENTION:  THERAPY AND DIAGNOSIS OF KIDNEY CANCER
;  FILE REFERENCE: 210121.572
;  CURRENT APPLICATION NUMBER: US/10/102,524
;  CURRENT FILING DATE:  2002-03-19
;  NUMBER OF SEQ ID NOS: 1863
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 307
;   LENGTH: 434
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 44, 177, 178
;   OTHER INFORMATION: n = A,T,C or G
US-10-102-524-307

  Query Match             21.4%;  Score 29.8;  DB 15;  Length 434;
  Best Local Similarity   56.7%;  Pred. No. 12;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy          43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
               || ||||     || ||  || ||| |  ||| || || | |||  | || |  | |
Db         271 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 330

Qy         103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
               |||||| |    |  |  || | ||||||||||
Db         331 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 367


RESULT 25
US-10-102-524-540
; Sequence 540, Application US/10102524
; Publication No. US20030109434A1
; GENERAL INFORMATION:
;  APPLICANT: Algate, Paul A.
;  APPLICANT:  Mannion, Jane
;  APPLICANT:  Gaiger, Alexander
;  APPLICANT:  Gordon, Brian
;  APPLICANT:  Harlocker, Susan L.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
;  TITLE OF INVENTION:  THERAPY AND DIAGNOSIS OF KIDNEY CANCER
;  FILE REFERENCE: 210121.572
;  CURRENT APPLICATION NUMBER: US/10/102,524
;  CURRENT FILING DATE:  2002-03-19
;  NUMBER OF SEQ ID NOS: 1863
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 540
;   LENGTH: 434
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-102-524-540

  Query Match             21.4%;  Score 29.8;  DB 15;  Length 434;
  Best Local Similarity   56.7%;  Pred. No. 12;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy          43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
               || ||||     || ||  || ||| |  ||| || || | |||  | || |  | |
Db         271 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 330

Qy         103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
               |||||| |    |  |  || | ||||||||||
Db         331 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 367


RESULT 26
US-10-027-632-81146
; Sequence 81146, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 81146
;   LENGTH: 444
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-81146

  Query Match             21.4%;  Score 29.8;  DB 13;  Length 444;
  Best Local Similarity   56.7%;  Pred. No. 12;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy          31 CTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTT 90
               | || |||| ||   ||    | || |   ||| ||  ||   || |  |  ||||||||
Db         318 CAGCTTCACTCTTGCTTACATATAAGGTCTGTGGCTGCTTTCATGCTACAACAACTGTTT 377

Qy          91 ATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTT 127
               |||||  ||   | | |||  |  |||  | | | ||
Db         378 ATCCCACAAAGCCTAAAATATATACTATCCAGATTTT 414


RESULT 27
US-10-027-632-81146
; Sequence 81146, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 81146
;   LENGTH: 444
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-81146
```

```
  Query Match             21.4%;  Score 29.8;  DB 15;  Length 444;
  Best Local Similarity   56.7%;  Pred. No. 12;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         31 CTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTT 90
              | || |||| ||   ||    | || |   ||| ||  ||   || |  | ||||||||
Db        318 CAGCTTCACTCTTGCTTACATATAAGGTCTGTGGCTGCTTTCATGCTACAACAACTGTTT 377

Qy         91 ATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTT 127
              |||||  ||   | | |||  |  |||  | | | ||
Db        378 ATCCCACAAAGCCTAAAATATATACTATCCAGATTTT 414


RESULT 28
US-10-027-632-109769
; Sequence 109769, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 109769
;   LENGTH: 463
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-109769

  Query Match             21.4%;  Score 29.8;  DB 13;  Length 463;
  Best Local Similarity   56.7%;  Pred. No. 12;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         31 CTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTT 90
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Db        366 CAGCTTCACTCTTGCTTACATATAAGGTCTGTGGCTGCTTTCATGCTACAACAACTGTTT 425

Qy         91 ATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTT 127
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Db        426 ATCCCACAAAGCCTAAAATATATACTATCCAGATTTT 462


RESULT 29
US-10-027-632-109769
; Sequence 109769, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 109769
;   LENGTH: 463
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-109769

  Query Match             21.4%;  Score 29.8;  DB 15;  Length 463;
  Best Local Similarity   56.7%;  Pred. No. 12;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         31 CTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTT 90
              | || |||| ||   ||    | || |   ||| ||  ||   || |  | ||||||||
Db        366 CAGCTTCACTCTTGCTTACATATAAGGTCTGTGGCTGCTTTCATGCTACAACAACTGTTT 425

Qy         91 ATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTT 127
              |||||  ||   | | |||  |  |||  | | | ||
Db        426 ATCCCACAAAGCCTAAAATATATACTATCCAGATTTT 462


RESULT 30
US-09-954-456-46
; Sequence 46, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cance
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-76
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/233,617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,052
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,923
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,637
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,638
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,711
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,720
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,840
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,863
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 2276
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
;   LENGTH: 492
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: n=a,t,g or c
US-09-954-456-46
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Query Match 21.4%; Score 29.8; DB 9; Length 492;
Best Local Similarity 56.7%; Pred. No. 12;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

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Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
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Db         77 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 136

Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
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Db        137 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 173
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 22, 2004, 01:50:26 ; Search time 66 Seconds
(without alignments)
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Title: US-10-070-882A-2
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Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	29.8	21.4	301	3	US-09-352-616A-293	Sequence 293, App
	3	29.8	21.4	301	4	US-09-232-149A-293	Sequence 293, App
	4	29.8	21.4	301	4	US-09-159-812-293	Sequence 293, App
	5	29.8	21.4	301	4	US-09-636-215-293	Sequence 293, App
	6	29.8	21.4	301	4	US-09-685-166A-293	Sequence 293, App
	7	29.8	21.4	301	4	US-09-688-489-293	Sequence 293, App
	8	29.8	21.4	301	4	US-09-679-426-293	Sequence 293, App
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	13	29	20.9	3010	3	US-08-714-918-71	Sequence 71, Appl
	14	29	20.9	3010	3	US-09-265-315-71	Sequence 71, Appl
	15	29	20.9	3010	3	US-09-265-315-71	Sequence 71, Appl
	16	29	20.9	3010	3	US-09-266-417-71	Sequence 71, Appl
	17	29	20.9	3010	4	US-09-528-709-71	Sequence 71, Appl
	18	29	20.9	3010	4	US-09-527-745-71	Sequence 71, Appl
c	19	28.8	20.7	2347	1	US-08-453-695A-113	Sequence 113, App
c	20	28.8	20.7	2347	1	US-08-268-161A-113	Sequence 113, App
c	21	28.8	20.7	2347	2	US-08-453-702A-113	Sequence 113, App
c	22	28.8	20.7	2347	3	US-09-099-639-113	Sequence 113, App
c	23	28.8	20.7	2347	5	PCT-US95-08071-113	Sequence 113, App
c	24	28.6	20.6	2676	3	US-09-212-971-11	Sequence 11, Appl
c	25	28.6	20.6	2676	3	US-08-800-929A-11	Sequence 11, Appl
c	26	28.6	20.6	2676	3	US-09-617-053A-11	Sequence 11, Appl
c	27	28.6	20.6	16397	4	US-08-956-171E-205	Sequence 205, App
c	28	28.6	20.6	16397	4	US-08-781-986A-205	Sequence 205, App
	29	28.4	20.4	1092	4	US-10-138-701-1	Sequence 1, Appli
c	30	28.4	20.4	1320	1	US-08-599-252-84	Sequence 84, Appl
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	36	28.4	20.4	5549	4	US-08-956-171E-188	Sequence 188, App
	37	28.4	20.4	5549	4	US-08-781-986A-188	Sequence 188, App
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	39	28.2	20.3	1242	4	US-09-328-352-1734	Sequence 1734, Ap
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c	41	28	20.1	1664976	4	US-09-692-570-1	Sequence 1, Appli
c	42	27.6	19.9	1815	4	US-09-436-521A-3	Sequence 3, Appli
c	43	27.2	19.6	3116	4	US-09-311-021-187	Sequence 187, App
c	44	27.2	19.6	4210	4	US-09-710-279-3761	Sequence 3761, Ap
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c	48	27	19.4	2431	3	US-08-714-918-15	Sequence 15, Appl
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c	53	27	19.4	2431	4	US-09-527-745-15	Sequence 15, Appl
	54	27	19.4	5544	4	US-08-956-171E-110	Sequence 110, App
	55	27	19.4	5544	4	US-08-781-986A-110	Sequence 110, App
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	57	27	19.4	90050	4	US-09-358-055B-5	Sequence 5, Appli
	58	27	19.4	90050	4	US-09-893-238-5	Sequence 5, Appli
	59	27	19.4	118999	4	US-09-791-105B-32	Sequence 32, Appl
	60	26.8	19.3	306	4	US-09-710-279-75	Sequence 75, Appl
	61	26.8	19.3	1319	3	US-09-200-934-3	Sequence 3, Appli
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	63	26.8	19.3	99916	4	US-09-816-095-3	Sequence 3, Appli
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c	65	26.6	19.1	273	4	US-09-513-999C-30229	Sequence 30229, A
	66	26.6	19.1	513	4	US-09-134-000C-109	Sequence 109, App
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c	71	26.6	19.1	2272	1	US-08-233-005-1	Sequence 1, Appli
c	72	26.6	19.1	2272	1	US-08-428-943-1	Sequence 1, Appli
c	73	26.6	19.1	2272	3	US-09-016-649-1	Sequence 1, Appli
c	74	26.6	19.1	2272	5	PCT-US95-04858-1	Sequence 1, Appli
	75	26.6	19.1	14759	4	US-09-661-887-1	Sequence 1, Appli
	76	26.6	19.1	1664976	4	US-08-916-421B-1	Sequence 1, Appli
	77	26.6	19.1	1664976	4	US-09-692-570-1	Sequence 1, Appli
	78	26.6	19.1	1830121	4	US-09-557-884-1	Sequence 1, Appli
	79	26.6	19.1	1830121	4	US-09-643-990A-1	Sequence 1, Appli
	80	26.6	19.1	1830121	4	US-10-329-960-1	Sequence 1, Appli
c	81	26.4	19.0	204	3	US-09-134-001C-2473	Sequence 2473, Ap
c	82	26.4	19.0	630	4	US-09-248-796A-3074	Sequence 3074, Ap
c	83	26.4	19.0	35100	1	US-08-306-691B-19	Sequence 19, Appl
c	84	26.4	19.0	35100	5	PCT-US93-06251-19	Sequence 19, Appl
c	85	26.2	18.8	250	4	US-09-270-767-26700	Sequence 26700, A
c	86	26.2	18.8	505	4	US-09-621-976-12828	Sequence 12828, A
c	87	26.2	18.8	746	4	US-09-270-767-11168	Sequence 11168, A
c	88	26	18.7	1404	3	US-09-134-001C-398	Sequence 398, App
c	89	26	18.7	1419	4	US-09-710-279-1901	Sequence 1901, Ap
c	90	26	18.7	2986	4	US-09-710-279-4365	Sequence 4365, Ap
	91	25.8	18.6	230	4	US-09-513-999C-34365	Sequence 34365, A
	92	25.8	18.6	330	1	US-08-450-944-6	Sequence 6, Appli
	93	25.8	18.6	330	5	PCT-US96-07709-6	Sequence 6, Appli
c	94	25.8	18.6	330	5	PCT-US96-07709-16	Sequence 16, Appl
c	95	25.8	18.6	396	4	US-09-621-976-15733	Sequence 15733, A
	96	25.8	18.6	905	5	PCT-US96-07709-24	Sequence 24, Appl
c	97	25.8	18.6	905	5	PCT-US96-07709-26	Sequence 26, Appl
	98	25.8	18.6	1002	3	US-09-134-001C-1109	Sequence 1109, Ap
	99	25.8	18.6	2229	4	US-09-494-297A-3	Sequence 3, Appli
c	100	25.8	18.6	3572	4	US-09-710-279-3527	Sequence 3527, Ap

ALIGNMENTS

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RESULT 1
US-09-439-313-293
; Sequence 293, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan Louise
;  APPLICANT:  Jiang Yuqui
;  APPLICANT:  Reed, Steven G.
;  APPLICANT:  Kalos, Michael
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Retter, Mark
;  APPLICANT:  Solk, John
;  APPLICANT:  Day, Craig
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C9
;  CURRENT APPLICATION NUMBER: US/09/439,313
;  CURRENT FILING DATE:  1999-11-12
;  NUMBER OF SEQ ID NOS: 575
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 293
;   LENGTH: 301
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-439-313-293

  Query Match             21.4%;  Score 29.8;  DB 3;  Length 301;
  Best Local Similarity   56.7%;  Pred. No. 0.43;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
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Db         30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
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Db         90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126


RESULT 2
US-09-352-616A-293
; Sequence 293, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Harlocker, Susan Louise
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Mitcham, Jennifer Lynn
;  TITLE OF INVENTION:  COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
;  TITLE OF INVENTION:  OF PROSTATE CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE:  210121.427C8
;  CURRENT APPLICATION NUMBER: US/09/352,616A
;  CURRENT FILING DATE:  1999-07-13
;  NUMBER OF SEQ ID NOS:  472
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 293
;   LENGTH: 301
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-352-616A-293

  Query Match             21.4%;  Score 29.8;  DB 3;  Length 301;
  Best Local Similarity   56.7%;  Pred. No. 0.43;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
              || ||||     || ||  || ||| |  ||| || || | |||  | || |  | |
Db         30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
              |||||| |    |  |  || | ||||||||||
Db         90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126


RESULT 3
US-09-232-149A-293
; Sequence 293, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer Lynn
;  TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
;  TITLE OF INVENTION:  CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.427C6
;  CURRENT APPLICATION NUMBER: US/09/232,149A
;  CURRENT FILING DATE:  1999-01-15
;  NUMBER OF SEQ ID NOS: 338
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 293
;   LENGTH: 301
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-232-149A-293

  Query Match             21.4%;  Score 29.8;  DB 4;  Length 301;
  Best Local Similarity   56.7%;  Pred. No. 0.43;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
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Db         30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
              |||||| |    |  |  || | ||||||||||
Db         90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126


RESULT 4
US-09-159-812-293
; Sequence 293, Application US/09159812A
; Patent No. 6613872
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT: Dillon, Davin C.
;  TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
;  TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.428C5
;  CURRENT APPLICATION NUMBER: US/09/159,812A
;  CURRENT FILING DATE: 1998-09-23
;  NUMBER OF SEQ ID NOS: 306
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 293
;   LENGTH: 301
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-159-812-293

  Query Match             21.4%;  Score 29.8;  DB 4;  Length 301;
  Best Local Similarity   56.7%;  Pred. No. 0.43;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
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Db         30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
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Db         90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126


RESULT 5
US-09-636-215-293
; Sequence 293, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.42717C17
;  CURRENT APPLICATION NUMBER: US/09/636,215
;  CURRENT FILING DATE:  2000-08-10
;  NUMBER OF SEQ ID NOS:  852
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 293
;   LENGTH: 301
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-636-215-293

  Query Match             21.4%;  Score 29.8;  DB 4;  Length 301;
  Best Local Similarity   56.7%;  Pred. No. 0.43;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy          43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
               || ||||     || ||  || ||| |  ||| || || | |||  | || |  | |
Db          30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy         103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
                 |||||| |    |  |  || | ||||||||||
Db          90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126


RESULT 6
US-09-685-166A-293
; Sequence 293, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C21
;  CURRENT APPLICATION NUMBER: US/09/685,166A
;  CURRENT FILING DATE:  2000-10-10
;  NUMBER OF SEQ ID NOS: 898
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 293
;   LENGTH: 301
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-685-166A-293

  Query Match             21.4%;  Score 29.8;  DB 4;  Length 301;
  Best Local Similarity   56.7%;  Pred. No. 0.43;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy          43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
               || ||||     || ||  || ||| |  ||| || || | |||  | || |  | |
Db          30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy         103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
                 |||||| |    |  |  || | ||||||||||
Db          90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126


RESULT 7
US-09-688-489-293
; Sequence 293, Application US/09688489
; Patent No. 6664377
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer Lynn
;  TITLE OF INVENTION:  COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
;  TITLE OF INVENTION:  CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE:  210121.427D2
;  CURRENT APPLICATION NUMBER: US/09/688,489
;  CURRENT FILING DATE:  2000-10-13
;  NUMBER OF SEQ ID NOS:  338
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 293
;   LENGTH: 301
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-688-489-293

  Query Match             21.4%;  Score 29.8;  DB 4;  Length 301;
  Best Local Similarity   56.7%;  Pred. No. 0.43;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy          43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
               || ||||     || ||  || ||| |  ||| || || | |||  | || |  | |
Db          30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy         103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
                 |||||| |    |  |  || | ||||||||||
Db          90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126


RESULT 8
US-09-679-426-293
; Sequence 293, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
```

```
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.427C20
;  CURRENT APPLICATION NUMBER: US/09/679,426
;  CURRENT FILING DATE:  2000-10-02
;  NUMBER OF SEQ ID NOS:  895
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 293
;   LENGTH: 301
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-679-426-293

  Query Match             21.4%;  Score 29.8;  DB 4;  Length 301;
  Best Local Similarity   56.7%;  Pred. No. 0.43;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
              || ||||     || ||  || ||| |  ||| || || | |||  | || |  | |
Db         30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
                 ||||||  |    |  |  || | ||||||||||
Db         90 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 126


RESULT 9
US-09-107-532A-1865/c
; Sequence 1865, Application US/09107532A
; Patent No. 6583275
;   GENERAL INFORMATION:
;        APPLICANT: Lynn A Doucette-Stamm  and David Bush
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                            ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;        NUMBER OF SEQUENCES: 7310
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;             STREET: 100 Beaver Street
;             CITY: Waltham
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02354
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD/ROM ISO9660
;             COMPUTER: PC
;             OPERATING SYSTEM: <Unknown>
;             SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/107,532A
;             FILING DATE: 30-Jun-1998
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/085,598
;             FILING DATE: 14 May 1998
;             APPLICATION NUMBER: 60/051571
;             FILING DATE: July 2, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ariniello, Pamela Deneke
;             REGISTRATION NUMBER: 40,489
;             REFERENCE/DOCKET NUMBER: GTC-012
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (781)893-5007
;             TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 1865:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1140 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: circular
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        ORIGINAL SOURCE:
;             ORGANISM: Enterococcus faecium
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION: (B) LOCATION 1...1140
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1865:
US-09-107-532A-1865

  Query Match             21.4%;  Score 29.8;  DB 4;  Length 1140;
  Best Local Similarity   66.2%;  Pred. No. 0.76;
  Matches   43;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy         30 CCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTT 89
              |||   |||||| ||| |  || || || || | |  |||| ||| |   |||| || |
Db        431 CCTAGTTCACCCACTTCTTCTCCGACAGTGGCTAATAATTTGACTGTTCCGTTAAATGGT 372

Qy         90 TATCC 94
              | |||
Db        371 TTTCC 367


RESULT 10
US-09-673-395A-82/c
; Sequence 82, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
;  APPLICANT: SPECHT, THOMAS
;  APPLICANT:  HINZMANN, BERND
;  APPLICANT:  SCHMITT, ARMIN
;  APPLICANT:  PILARSKY, CHRISTIAN
;  APPLICANT:  DAHL, EDGAR
;  APPLICANT:  ROSENTHAL, ANDRE
;  TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
;  FILE REFERENCE: ALBRE-12
;  CURRENT APPLICATION NUMBER: US/09/673,395A
;  CURRENT FILING DATE:  2000-10-17
;  NUMBER OF SEQ ID NOS: 637
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
;   LENGTH: 2143
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-673-395A-82

  Query Match             21.4%;  Score 29.8;  DB 4;  Length 2143;
  Best Local Similarity   56.7%;  Pred. No. 1;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
              || ||||     || ||  || ||| |  ||| || || | |||  | || |  | |
Db       1254 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 1195

Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
                 ||||||  |    |  |  || | ||||||||||
Db       1194 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 1158


RESULT 11
US-09-489-847-86
; Sequence 86, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al
;  TITLE OF INVENTION: 98 Human Secreted Proteins
;  FILE REFERENCE: PZ031P1
```

```
;  CURRENT APPLICATION NUMBER: US/09/489,847
;  CURRENT FILING DATE: 2000-01-24
;  EARLIER APPLICATION NUMBER: PCT/US99/17130
;  EARLIER FILING DATE: 1999-07-29
;  EARLIER APPLICATION NUMBER: 60/094,657
;  EARLIER FILING DATE: 1998-07-30
;  EARLIER APPLICATION NUMBER: 60/095,486
;  EARLIER FILING DATE: 1998-08-05
;  EARLIER APPLICATION NUMBER: 60/096,319
;  EARLIER FILING DATE: 1998-08-12
;  EARLIER APPLICATION NUMBER: 60/095,454
;  EARLIER FILING DATE: 1998-08-06
;  EARLIER APPLICATION NUMBER: 60/095,455
;  EARLIER FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 376
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
;   LENGTH: 3174
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-489-847-86

  Query Match             21.4%;  Score 29.8;  DB 4;  Length 3174;
  Best Local Similarity   56.7%;  Pred. No. 1.2;
  Matches   55;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy         43 CTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCA 102
              || ||||      || ||  || ||| |  ||| || || | |||  | || |  | |
Db       1767 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 1826

Qy        103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
              |||||| |    |  |  || | ||||||||||
Db       1827 AATCAATCAATGGCCTAGAGCACTGACTGTTAACACA 1863


RESULT 12
US-08-961-527-52/c
; Sequence 52, Application US/08961527
; Patent No. 6420135
;  GENERAL INFORMATION:
;    APPLICANT:  Charles Kunsch
;    TITLE OF INVENTION:  Streptococcus pneumoniae Polynucleotides and Sequences
;    NUMBER OF SEQUENCES:  391
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/961,527
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brookes, A. Anders
;      REGISTRATION NUMBER:  36,373
;      REFERENCE/DOCKET NUMBER:  PB340P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  52:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16593 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-961-527-52

  Query Match             21.0%;  Score 29.2;  DB 4;  Length 16593;
  Best Local Similarity   81.0%;  Pred. No. 3.9;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         39 CCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTA 80
              ||| | || |||||||| |  |||||||| |||||| |||
Db      12443 CCCACCTTCCTTCAGAATGCTGGTGACTATCTGTCTGGCTTA 12402


RESULT 13
US-08-714-918-71
; Sequence 71, Application US/08714918
; Patent No. 6037123
;  GENERAL INFORMATION:
;    APPLICANT:  Benton, Bret
;    APPLICANT:  Lee, Ving
;    APPLICANT:  Malouin, Francois
;    APPLICANT:  Martin, Patrick K.
;    APPLICANT:  Schmid, Molly B.
;    APPLICANT:  Sun, Dongxu
;    TITLE OF INVENTION:  STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
;    TITLE OF INVENTION:  TARGET GENES
;    NUMBER OF SEQUENCES:  111
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/714,918
;      FILING DATE:  September 13, 1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/009,102
;      FILING DATE:  December 22, 1995
;      APPLICATION NUMBER:  60/003,798
;      FILING DATE:  September 15, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  222/005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3010 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-714-918-71

  Query Match             20.9%;  Score 29;  DB 3;  Length 3010;
  Best Local Similarity   52.5%;  Pred. No. 2.2;
  Matches   62;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy          7 CTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACT 66
              ||| |  |    ||| ||||||  | ||  || | ||   |||| |||   ||  ||
Db       1119 CTGCTTTAGTCGCTTGAATAATTTCGGCAGCAACGTCAGGTCTTAAGATTAAGCCGGANC 1178
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```
Qy          67 ATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGACTGTT 124
               ||  |   ||||  |||  ||  | |    |     ||||| | ||  |||  |  ||
Db        1179 CCTTACCCTTTTTAGCAACATTTGCTACAGGACATCCCATATTTAAGTCTATGCCTTT 1236


RESULT 14
US-09-265-315-71
; Sequence 71, Application US/09265315
; Patent No. 6187541
;  GENERAL INFORMATION:
;    APPLICANT:  Benton, Bret
;    APPLICANT:  Lee, Ving J.
;    APPLICANT:  Malouin, Francois
;    APPLICANT:  Martin, Patrick K.
;    APPLICANT:  Schmid, Molly B.
;    APPLICANT:  Sun, Dongxu
;    TITLE OF INVENTION:  METHODS OF SCREENING FOR COMPOUNDS
;    TITLE OF INVENTION:  ACTIVE ON STAPHYLOCOCCUS AUREUS
;    TITLE OF INVENTION:  TARGET GENES
;    NUMBER OF SEQUENCES:  111
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/265,315
;      FILING DATE:  March 9, 1999
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/714,918
;      FILING DATE:  September 13, 1996
;      APPLICATION NUMBER:  60/009,102
;      FILING DATE:  December 22, 1995
;      APPLICATION NUMBER:  60/003,798
;      FILING DATE:  September 15, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  240/247
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3010 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-265-315-71

  Query Match           20.9%;  Score 29;  DB 3;  Length 3010;
  Best Local Similarity   52.5%;  Pred. No. 2.2;
  Matches   62;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy           7 CTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACT 66
               ||| |  |   ||| ||||||  | ||  || | ||   |||| |||   ||   ||
Db        1119 CTGCTTTAGTCGCTTGAATAATTTCGGCAGCAACGTCAGGTCTTAAGATTAAGCCGGANC 1178

Qy          67 ATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGACTGTT 124
               ||  |   ||||  |||  ||  | |    |     ||||| | ||  |||  |  ||
Db        1179 CCTTACCCTTTTTAGCAACATTTGCTACAGGACATCCCATATTTAAGTCTATGCCTTT 1236


RESULT 15
US-09-265-315-71
; Sequence 71, Application US/09265315
; Patent No. 6187541
;  GENERAL INFORMATION:
;    APPLICANT:  Benton, Bret
;    APPLICANT:  Lee, Ving J.
;    APPLICANT:  Malouin, Francois
;    APPLICANT:  Martin, Patrick K.
;    APPLICANT:  Schmid, Molly B.
;    APPLICANT:  Sun, Dongxu
;    TITLE OF INVENTION:  METHODS OF SCREENING FOR COMPOUNDS
;    TITLE OF INVENTION:  ACTIVE ON STAPHYLOCOCCUS AUREUS
;    TITLE OF INVENTION:  TARGET GENES
;    NUMBER OF SEQUENCES:  111
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/265,315
;      FILING DATE:  March 9, 1999
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/714,918
;      FILING DATE:  September 13, 1996
;      APPLICATION NUMBER:  60/009,102
;      FILING DATE:  December 22, 1995
;      APPLICATION NUMBER:  60/003,798
;      FILING DATE:  September 15, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  240/247
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3010 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-265-315-71

  Query Match           20.9%;  Score 29;  DB 3;  Length 3010;
  Best Local Similarity   52.5%;  Pred. No. 2.2;
  Matches   62;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy           7 CTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACT 66
               ||| |  |   ||| ||||||  | ||  || | ||   |||| |||   ||   ||
Db        1119 CTGCTTTAGTCGCTTGAATAATTTCGGCAGCAACGTCAGGTCTTAAGATTAAGCCGGANC 1178

Qy          67 ATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGACTGTT 124
               ||  |   ||||  |||  ||  | |    |     ||||| | ||  |||  |  ||
Db        1179 CCTTACCCTTTTTAGCAACATTTGCTACAGGACATCCCATATTTAAGTCTATGCCTTT 1236


RESULT 16
US-09-266-417-71
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; Sequence 71, Application US/09266417
; Patent No. 6228588
;  GENERAL INFORMATION:
;    APPLICANT:  Benton, Bret
;    APPLICANT:  Lee, Ving J.
;    APPLICANT:  Malouin, Francois
;    APPLICANT:  Martin, Patrick K.
;    APPLICANT:  Schmid, Molly B.
;    APPLICANT:  Sun, Dongxu
;    TITLE OF INVENTION:  METHODS OF SCREENING FOR COMPOUNDS
;    TITLE OF INVENTION:  ACTIVE ON STAPHYLOCOCCUS AUREUS
;    TITLE OF INVENTION:  TARGET GENES
;    NUMBER OF SEQUENCES:  111
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/266,417
;      FILING DATE:  March 9, 1999
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/714,918
;      FILING DATE:  September 13, 1996
;      APPLICATION NUMBER:  60/009,102
;      FILING DATE:  December 22, 1995
;      APPLICATION NUMBER:  60/003,798
;      FILING DATE:  September 15, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  240/248
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3010 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-266-417-71

  Query Match             20.9%;  Score 29;  DB 3;  Length 3010;
  Best Local Similarity   52.5%;  Pred. No. 2.2;
  Matches   62;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy          7 CTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACT 66
              ||| |  |    ||| ||||||  | ||  || | ||   |||| |||   ||   ||
Db       1119 CTGCTTTAGTCGCTTGAATAATTTCGGCAGCAACGTCAGGTCTTAAGATTAAGCCGGANC 1178

Qy         67 ATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGACTGTT 124
                ||  |   ||||  |||  ||  | |   |    |||| | ||  |||  |  ||
Db       1179 CCTTACCCTTTTTAGCAACATTTGCTACAGGACATCCCATATTTAAGTCTATGCCTTT 1236


RESULT 17
US-09-528-709-71
; Sequence 71, Application US/09528709
; Patent No. 6630303
;  GENERAL INFORMATION:
;       APPLICANT: Benton, Bret
;                  Lee, Ving
;                  Malouin, Francois
;                  Martin, Patrick K.
;                  Schmid, Molly B.
;                  Sun, Dongxu
;       TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
;                           TARGET GENES
;       NUMBER OF SEQUENCES: 111
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Lyon & Lyon
;            STREET: 633 West Fifth Street
;                    Suite 4700
;            CITY: Los Angeles
;            STATE: California
;            COUNTRY: U.S.A.
;            ZIP: 90071-2066
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                         storage
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: IBM P.C. DOS 5.0
;            SOFTWARE: Word Perfect 5.1
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/528,709
;            FILING DATE: 17-Mar-2000
;            CLASSIFICATION: 424
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/714,918
;            FILING DATE: September 13, 1996
;            APPLICATION NUMBER: 60/009,102
;            FILING DATE: December 22, 1995
;            APPLICATION NUMBER: 60/003,798
;            FILING DATE: September 15, 1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Warburg, Richard J.
;            REGISTRATION NUMBER: 32,327
;            REFERENCE/DOCKET NUMBER: 222/005
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (213) 489-1600
;            TELEFAX: (213) 955-0440
;            TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 71:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 3010 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-09-528-709-71

  Query Match             20.9%;  Score 29;  DB 4;  Length 3010;
  Best Local Similarity   52.5%;  Pred. No. 2.2;
  Matches   62;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy          7 CTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACT 66
              ||| |  |    ||| ||||||  | ||  || | ||   |||| |||   ||   ||
Db       1119 CTGCTTTAGTCGCTTGAATAATTTCGGCAGCAACGTCAGGTCTTAAGATTAAGCCGGANC 1178

Qy         67 ATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGACTGTT 124
                ||  |   ||||  |||  ||  | |   |    |||| | ||  |||  |  ||
Db       1179 CCTTACCCTTTTTAGCAACATTTGCTACAGGACATCCCATATTTAAGTCTATGCCTTT 1236


RESULT 18
US-09-527-745-71
; Sequence 71, Application US/09527745
; Patent No. 6638718
;  GENERAL INFORMATION:
;       APPLICANT: Benton, Bret
;                  Lee, Ving
;                  Malouin, Francois
;                  Martin, Patrick K.
;                  Schmid, Molly B.
```

```
;                  Sun, Dongxu
;       TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
;                           TARGET GENES
;       NUMBER OF SEQUENCES: 111
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Lyon & Lyon
;            STREET: 633 West Fifth Street
;                    Suite 4700
;            CITY: Los Angeles
;            STATE: California
;            COUNTRY: U.S.A.
;            ZIP: 90071-2066
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                         storage
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: IBM P.C. DOS 5.0
;            SOFTWARE: Word Perfect 5.1
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/527,745
;            FILING DATE: 17-Mar-2000
;            CLASSIFICATION: 424
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/714,918
;            FILING DATE: September 13, 1996
;            APPLICATION NUMBER: 60/009,102
;            FILING DATE: December 22, 1995
;            APPLICATION NUMBER: 60/003,798
;            FILING DATE: September 15, 1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Warburg, Richard J.
;            REGISTRATION NUMBER: 32,327
;            REFERENCE/DOCKET NUMBER: 222/005
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (213) 489-1600
;            TELEFAX: (213) 955-0440
;            TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 71:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 3010 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-09-527-745-71

  Query Match             20.9%;  Score 29;  DB 4;  Length 3010;
  Best Local Similarity   52.5%;  Pred. No. 2.2;
  Matches   62;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy          7 CTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACT 66
              ||| |  |    ||| ||||||  | ||  || | ||   |||| |||   ||   ||
Db       1119 CTGCTTTAGTCGCTTGAATAATTTCGGCAGCAACGTCAGGTCTTAAGATTAAGCCGGANC 1178

Qy         67 ATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGACTGTT 124
                ||  |   ||||  |||  ||  | |   |    |||| | ||  |||  |  ||
Db       1179 CCTTACCCTTTTTAGCAACATTTGCTACAGGACATCCCATATTTAAGTCTATGCCTTT 1236


RESULT 19
US-08-453-695A-113/c
; Sequence 113, Application US/08453695A
; Patent No. 5708143
;  GENERAL INFORMATION:
;    APPLICANT:  Suzuki, Shintaro
;    TITLE OF INVENTION:  Protocadherin Materials and Methods
;    NUMBER OF SEQUENCES:  115
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray, &
;      ADDRESSEE:  Borun
;      STREET:  233 South Wacker, 6300 Sears Tower
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/453,695A
;      FILING DATE:
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5708143and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  32658
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  113:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2347 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-453-695A-113

  Query Match             20.7%;  Score 28.8;  DB 1;  Length 2347;
  Best Local Similarity   60.0%;  Pred. No. 2.3;
  Matches   48;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy         56 AGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGC 115
              ||| || |||| ||| || |    | ||  |   | || ||||   |  ||||| | |
Db        366 AGATGGAGACTTTTTCTCGGTCCAAATATTTCCATGTCACCAATCTATAATAATTATCTA 307

Qy        116 TAGACTGTTCTTATTGTTAA 135
              | |||| |||| |||   ||
Db        306 TTGACTTTTCTAATTTAAAA 287


RESULT 20
US-08-268-161A-113/c
; Sequence 113, Application US/08268161A
; Patent No. 5798224
;  GENERAL INFORMATION:
;    APPLICANT:  Suzuki, Shintaro
;    TITLE OF INVENTION:  Protocadherin Materials and Methods
;    NUMBER OF SEQUENCES:  115
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray, &
;      ADDRESSEE:  Borun
;      STREET:  233 South Wacker, 6300 Sears Tower
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/268,161A
;      FILING DATE:  June 27, 1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Young J. Suh
;      REGISTRATION NUMBER:  P-41,337
;      REFERENCE/DOCKET NUMBER:  27866/32149
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
```

```
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  113:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2347 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-268-161A-113

  Query Match             20.7%;  Score 28.8;  DB 1;  Length 2347;
  Best Local Similarity   60.0%;  Pred. No. 2.3;
  Matches   48;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy         56 AGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGC 115
              ||| || |||| ||| || |    | ||  |   | || ||||   |  ||||| | |
Db        366 AGATGGAGACTTTTTCTCGGTCCAAATATTTCCATGTCACCAATCTATAATAATTATCTA 307

Qy        116 TAGACTGTTCTTATTGTTAA 135
              | |||| |||| |||   ||
Db        306 TTGACTTTTCTAATTTAAAA 287


RESULT 21
US-08-453-702A-113/c
; Sequence 113, Application US/08453702A
; Patent No. 5891706
;  GENERAL INFORMATION:
;    APPLICANT:  Suzuki, Shintaro
;    TITLE OF INVENTION:  Protocadherin Materials and Methods
;    NUMBER OF SEQUENCES:  115
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray, &
;      ADDRESSEE:  Borun
;      STREET:  233 South Wacker, 6300 Sears Tower
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/453,702A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5891706and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  32657
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  113:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2347 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-453-702A-113

  Query Match             20.7%;  Score 28.8;  DB 2;  Length 2347;
  Best Local Similarity   60.0%;  Pred. No. 2.3;
  Matches   48;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy         56 AGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGC 115
              ||| || |||| ||| || |    | ||  |   | || ||||   |  ||||| | |
Db        366 AGATGGAGACTTTTTCTCGGTCCAAATATTTCCATGTCACCAATCTATAATAATTATCTA 307

Qy        116 TAGACTGTTCTTATTGTTAA 135
              | |||| |||| |||   ||
Db        306 TTGACTTTTCTAATTTAAAA 287


RESULT 22
US-09-099-639-113/c
; Sequence 113, Application US/09099639
; Patent No. 6262237
;  GENERAL INFORMATION:
;    APPLICANT:  Suzuki, Shintaro
;    TITLE OF INVENTION:  Protocadherin Materials and Methods
;    NUMBER OF SEQUENCES:  115
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray, &
;      STREET:  233 South Wacker, 6300 Sears Tower
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Patent In Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/099,639
;      FILING DATE:  18 JUN 1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/263,161
;      FILING DATE:  27 JUN 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Greta E. No. 6262237and
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  27866/34703
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  113:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2347 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-099-639-113

  Query Match             20.7%;  Score 28.8;  DB 3;  Length 2347;
  Best Local Similarity   60.0%;  Pred. No. 2.3;
  Matches   48;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy         56 AGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGC 115
              ||| || |||| ||| || |    | ||  |   | || ||||   |  ||||| | |
Db        366 AGATGGAGACTTTTTCTCGGTCCAAATATTTCCATGTCACCAATCTATAATAATTATCTA 307

Qy        116 TAGACTGTTCTTATTGTTAA 135
              | |||| |||| |||   ||
Db        306 TTGACTTTTCTAATTTAAAA 287


RESULT 23
PCT-US95-08071-113/c
; Sequence 113, Application PC/TUS9508071
;  GENERAL INFORMATION:
;    APPLICANT:  Suzuki, Shintaro
;    TITLE OF INVENTION:  Protocadherin Materials and Methods
;    NUMBER OF SEQUENCES:  115
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray, &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 S. Wacker Drive
```

```
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/08071
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/12588
;      FILING DATE:  23 DEC 1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/998,003
;      FILING DATE:  29 DEC 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Noland, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  32149
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  113:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2347 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
PCT-US95-08071-113

  Query Match             20.7%;  Score 28.8;  DB 5;  Length 2347;
  Best Local Similarity   60.0%;  Pred. No. 2.3;
  Matches   48;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy         56 AGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGC 115
              ||| || |||| ||| || |    | ||  |   | || ||||   |  ||||| | |
Db        366 AGATGGAGACTTTTTCTCGGTCCAAATATTTCCATGTCACCAATCTATAATAATTATCTA 307

Qy        116 TAGACTGTTCTTATTGTTAA 135
              | |||| |||| |||   ||
Db        306 TTGACTTTTCTAATTTAAAA 287


RESULT 24
US-09-212-971-11/c
; Sequence 11, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
;  APPLICANT: Korneluk, Robert G
;  APPLICANT: MacKenzie, Alexander E
;  APPLICANT: Liston, Peter
;  APPLICANT: Baird, Stephen
;  APPLICANT: Tsang, Benjamin K
;  APPLICANT: Pratt, Christine
;  TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
;  TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
;  TITLE OF INVENTION: DISEASE
;  FILE REFERENCE: 07891/009002
;  CURRENT APPLICATION NUMBER: US/09/212,971B
;  CURRENT FILING DATE: 1998-12-16
;  EARLIER APPLICATION NUMBER: 60/017,354
;  EARLIER FILING DATE: 1996-04-26
;  EARLIER APPLICATION NUMBER: 60/030,590
;  EARLIER FILING DATE: 1996-11-14
;  EARLIER APPLICATION NUMBER: 08/800,929
;  EARLIER FILING DATE: 1997-02-13
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 2676
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-212-971-11

  Query Match             20.6%;  Score 28.6;  DB 3;  Length 2676;
  Best Local Similarity   64.2%;  Pred. No. 2.9;
  Matches   43;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy         42 TCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGC 101
              | ||||||| | ||| |  | |   |||    || ||||||||||| ||| || | ||  |
Db       2671 TTTTTTCTTTAAAAAAAAAGAGGTAATTATGTTGCTTTATTAACTTTTTCTCACAAATTC 2612

Qy        102 ACCATAA 108
                ||||
Db       2611 TTTATAA 2605


RESULT 25
US-08-800-929A-11/c
; Sequence 11, Application US/08800929A
; Patent No. 6133437
;  GENERAL INFORMATION:
;    APPLICANT:  Korneluk, Robert G
;    APPLICANT:  MacKenzie, Alexander E
;    APPLICANT:  Liston, Peter
;    APPLICANT:  Baird, Stephen
;    APPLICANT:  Tsang, Benjamin K
;    APPLICANT:  Pratt, Christine
;    TITLE OF INVENTION:  DETECTION AND MODULATION OF
;    TITLE OF INVENTION:  IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
;    TITLE OF INVENTION:  DISEASE
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Clark & Elbing LLP
;      STREET:  176 Federal Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/800,929A
;      FILING DATE:  13-FEB-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/030,590
;      FILING DATE:  14-NOV-1996
;      APPLICATION NUMBER:  60/017,354
;      FILING DATE:  26-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bieker-Brady, Kristina
;      REGISTRATION NUMBER:
;      REFERENCE/DOCKET NUMBER:  07891/009001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-428-0200
;      TELEFAX:  617-428-7045
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2676 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-800-929A-11
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  Query Match            20.6%;  Score 28.6;  DB 3;  Length 2676;
  Best Local Similarity   64.2%;  Pred. No. 2.9;
  Matches   43;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy         42 TCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGC 101
              | ||||||| | ||| |  | |   |||    || ||||||||||| ||| || | ||  |
Db       2671 TTTTTTCTTTAAAAAAAAAGAGGTAATTATGTTGCTTTATTAACTTTTTCTCACAAATTC 2612

Qy        102 ACCATAA 108
              ||||
Db       2611 TTTATAA 2605


RESULT 26
US-09-617-053A-11/c
; Sequence 11, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
;  APPLICANT: Korneluk, Robert G
;  APPLICANT:  MacKenzie, Alexander E
;  APPLICANT:  Liston, Peter
;  APPLICANT:  Baird, Stephen
;  APPLICANT:  Tsang, Benjamin K
;  APPLICANT:  Pratt, Christine
;  TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
;  TITLE OF INVENTION:  NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
;  TITLE OF INVENTION:  DISEASE
;  FILE REFERENCE: 07891/009003
;  CURRENT APPLICATION NUMBER: US/09/617,053A
;  CURRENT FILING DATE:  2000-07-14
;  PRIOR APPLICATION NUMBER: US 08/800,929
;  PRIOR FILING DATE: 1997-02-13
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 2676
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-617-053A-11

  Query Match            20.6%;  Score 28.6;  DB 3;  Length 2676;
  Best Local Similarity   64.2%;  Pred. No. 2.9;
  Matches   43;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy         42 TCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGC 101
              | ||||||| | ||| |  | |   |||    || ||||||||||| ||| || | ||  |
Db       2671 TTTTTTCTTTAAAAAAAAAGAGGTAATTATGTTGCTTTATTAACTTTTTCTCACAAATTC 2612

Qy        102 ACCATAA 108
              ||||
Db       2611 TTTATAA 2605


RESULT 27
US-08-956-171E-205/c
; Sequence 205, Application US/08956171E
; Patent No. 6593114
;   GENERAL INFORMATION:
;       APPLICANT: Charles Kunsch
;                  Gil H. Choi
;                  Patrick S. Dillon
;                  Craig A. Rosen
;                  Steven C. Barash
;                  Michael R. Fannon
;       TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;       NUMBER OF SEQUENCES: 5256
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Human Genome Sciences, Inc.
;            STREET: 9410 Key West Avenue
;            CITY: Rockville
;            STATE: Maryland
;            COUNTRY: USA
;            ZIP: 20850
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;            COMPUTER: HP Vectra 486/33
;            OPERATING SYSTEM: MSDOS version 6.2
;            SOFTWARE: ASCII Text
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/956,171E
;            FILING DATE: 20-Oct-1997
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/009,861
;            FILING DATE: January 5, 1996
;            APPLICATION NUMBER: 08/781,986
;            FILING DATE: January 3, 1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Mark J. Hyman
;            REGISTRATION NUMBER: 46,789
;            REFERENCE/DOCKET NUMBER: PB248P1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (240) 314-1224
;            TELEFAX: (301) 309-8439
;   INFORMATION FOR SEQ ID NO: 205:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 16397 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 205:
US-08-956-171E-205

  Query Match            20.6%;  Score 28.6;  DB 4;  Length 16397;
  Best Local Similarity   53.9%;  Pred. No. 6.3;
  Matches   55;  Conservative    1;  Mismatches   46;  Indels    0;  Gaps    0;

Qy         14 ACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTC 73
              || ||||||||||       |  | |       |||| ||| |  | ||||  |  |
Db       4185 ACTAACTTAAATATCAAACGTTTAATGGNAATTTCATCATACCGTGGGTATCCGTCACCG 4126

Qy         74 TGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGC 115
              | ||   ||| | |||  |   ||||  || | || |:||||
Db       4125 TCGTGGTTTACCAGTTCGTGGTCAAAAAACGAAAAACMACGC 4084


RESULT 28
US-08-781-986A-205/c
; Sequence 205, Application US/08781986A
; Patent No. 6737248
;  GENERAL INFORMATION:
;    APPLICANT:  Charles Kunsch
;    TITLE OF INVENTION:  Staphylococcus aureus Polynucleotides and Sequences
;    NUMBER OF SEQUENCES:  5255
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/781,986A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Benson, Bob
;      REGISTRATION NUMBER:  30,446
```

```
;      REFERENCE/DOCKET NUMBER:  PB248PP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  205:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16397 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-781-986A-205

  Query Match           20.6%;  Score 28.6;  DB 4;  Length 16397;
  Best Local Similarity  53.9%;  Pred. No. 6.3;
  Matches   55;  Conservative    1;  Mismatches   46;  Indels    0;  Gaps    0;

Qy         14 ACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTC 73
              || ||||||||||      |  | |      |||| ||| |  | ||||  |  |
Db       4185 ACTAACTTAAATATCAAACGTTTAATGGNAATTTCATCATACCGTGGGTATCCGTCACCG 4126

Qy         74 TGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGC 115
              | ||   ||| | |||  |   ||||  || | || |:||||
Db       4125 TCGTGGTTTACCAGTTCGTGGTCAAAAAACGAAAAACMACGC 4084


RESULT 29
US-10-138-701-1
; Sequence 1, Application US/10138701
; Patent No. 6753149
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.  et al.
;  TITLE OF INVENTION: Staphylococcus aureus genes and polypeptides
;  FILE REFERENCE: PB484
;  CURRENT APPLICATION NUMBER: US/10/138,701
;  CURRENT FILING DATE:  2002-05-06
;  PRIOR APPLICATION NUMBER: US/09/512,255A
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/098,964
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: US 60/009,861
;  PRIOR FILING DATE: 1996-01-05
;  PRIOR APPLICATION NUMBER: PCT/ US99/19726
;  PRIOR FILING DATE: 1999-08-31
;  PRIOR APPLICATION NUMBER: US 08/956,171
;  PRIOR FILING DATE: 1997-10-20
;  NUMBER OF SEQ ID NOS: 61
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 1092
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-138-701-1

  Query Match           20.4%;  Score 28.4;  DB 4;  Length 1092;
  Best Local Similarity  52.5%;  Pred. No. 2.3;
  Matches   62;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy         20 TTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTT 79
              | || |||| ||||          |||| || |||| | |   |||||      ||| |
Db         54 TAAATTAATACCTGGTATTAAAAATTTTATTAAGAAGGTGTTCAACTATGAACGTGGGTA 113

Qy         80 ATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTAACA 137
              | ||   |||    |  | || ||| ||   |   | |||  | | |||| | | ||
Db        114 TTAAAGGTTTTGGTGCATATGCGCCAGAAAAGATTATTGACAATGCCTATTTTGAGCA 171


RESULT 30
US-08-599-252-84/c
; Sequence 84, Application US/08599252
; Patent No. 5705343
;  GENERAL INFORMATION:
;    APPLICANT:  DRAYNA, DENNIS T.
;    APPLICANT:  FEDER, JOHN N.
;    APPLICANT:  GNIRKE, ANDREAS
;    APPLICANT:  KIMMEL, BRUCE E.
;    APPLICANT:  THOMAS, WINSTON J.
;    APPLICANT:  WOLFF, ROGER K.
;    TITLE OF INVENTION:  METHOD TO DIAGNOSE HEREDITARY
;    TITLE OF INVENTION:  HEMOCHROMATOSIS
;    NUMBER OF SEQUENCES:  124
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Ave. N.W., Suite 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/599,252
;      FILING DATE:  09-FEB-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  9053-0001.21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;      TELEX:  90-4030
;  INFORMATION FOR SEQ ID NO:  84:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1320 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-599-252-84

  Query Match           20.4%;  Score 28.4;  DB 1;  Length 1320;
  Best Local Similarity  50.7%;  Pred. No. 2.5;
  Matches   68;  Conservative    0;  Mismatches   66;  Indels    0;  Gaps    0;

Qy          2 TGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGG 61
              | | | |  || |  || || ||  |||| |   |     |    | ||| |   ||||
Db        304 TTATTTTTTTCTAGAAAGTTCAAATATGCTTTTATAGTGCCAAATGCTTGAATGAGAGCC 245

Qy         62 TGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGACT 121
              | ||  |   |   ||||  |  ||  |      | ||||||||||||  | || |
Db        244 AAAATAAATTGTTTAATTATCCAGCTTTAGTATATCCAACACCATAATCAACCGTGGATT 185

Qy        122 GTTCTTATTGTTAA 135
              | |  ||| | ||
Db        184 CTGCACATTTTGAA 171


Search completed: December 22, 2004, 03:32:09
Job time : 75 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 22, 2004, 01:40:57 ; Search time 1743 Seconds
(without alignments)
2905.980 Million cell updates/sec

Title: US-10-070-882A-2
Perfect score: 139
Sequence: 1 gtgactctggtcgacgaact.....ctgttcttattgttaacaca 139

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	34.8	25.0	3932	3	AK082454	AK082454 Mus muscu
	2	34.4	24.7	414	6	BY642267	BY642267 BY642267
	3	33.6	24.2	204	1	AV231406	AV231406 AV231406
	4	33.6	24.2	274	2	BB775700	BB775700 BB775700
	5	33.6	24.2	318	2	BB094276	BB094276 BB094276
	6	33.6	24.2	335	2	BB222962	BB222962 BB222962
	7	33.6	24.2	448	5	BY439440	BY439440 BY439440
c	8	33.6	24.2	570	8	AZ435636	AZ435636 1M0222H14
	9	33.6	24.2	590	2	BE131381	BE131381 L48-1355T
	10	33.6	24.2	605	4	BM658097	BM658097 MCR059H01
	11	33.6	24.2	625	6	CA835622	CA835622 MCS039B06
	12	33.6	24.2	633	6	CA834105	CA834105 MCS028H02
	13	33.6	24.2	674	4	BM301497	BM301497 MCR046F12
	14	33.6	24.2	699	4	BM301422	BM301422 MCR045F12
	15	33.6	24.2	746	9	CR303205	CR303205 Medicago
	16	33.6	24.2	863	2	BE035174	BE035174 MO22B09 M
	17	33.6	24.2	866	9	CR308064	CR308064 Medicago
	18	33.6	24.2	889	9	CG952370	CG952370 MBEAT30TR
	19	33.6	24.2	1192	2	BE037111	BE037111 MP15B07 M
c	20	33.4	24.0	521	8	AQ830244	AQ830244 HS_4825_B
	21	33.4	24.0	728	9	AG308530	AG308530 Mus muscu
c	22	33.4	24.0	957	6	CA791309	CA791309 AGENCOURT
	23	33.2	23.9	205	2	BB004186	BB004186 BB004186
	24	33	23.7	467	8	BZ915818	BZ915818 CH240_59A
	25	32.8	23.6	206	1	AV336201	AV336201 AV336201
c	26	32.8	23.6	690	8	BZ035953	BZ035953 oeh99d03.
	27	32.4	23.3	252	2	BB230680	BB230680 BB230680
	28	32.4	23.3	270	2	BB118576	BB118576 BB118576
	29	32.4	23.3	533	5	BY480819	BY480819 BY480819
	30	32.4	23.3	906	8	AQ781019	AQ781019 HS_3169_B
c	31	32.2	23.2	275	1	AI414763	AI414763 ma59d02.x
	32	32.2	23.2	459	2	BE289932	BE289932 601089159
	33	32.2	23.2	579	1	AI981576	AI981576 pat.pk006
	34	32.2	23.2	741	9	CC537179	CC537179 CH240_416
c	35	32.2	23.2	769	8	AQ869785	AQ869785 nbeb0035P
c	36	32	23.0	239	1	AA686653	AA686653 EST110929
	37	32	23.0	274	2	BB364524	BB364524 BB364524
	38	32	23.0	320	2	BB464866	BB464866 BB464866
	39	32	23.0	391	5	BY468249	BY468249 BY468249
c	40	32	23.0	490	8	AQ430313	AQ430313 HS_5093_A
	41	32	23.0	501	8	BH002081	BH002081 BMBAC02A1
c	42	32	23.0	611	7	CO040889	CO040889 UI-M-FW0-
	43	32	23.0	706	8	BH830539	BH830539 BACPP31-N
c	44	32	23.0	745	9	AG479014	AG479014 Mus muscu
	45	31.8	22.9	175	9	CE320783	CE320783 tigr-gss-
	46	31.8	22.9	312	1	AV258037	AV258037 AV258037
	47	31.8	22.9	312	2	BB026689	BB026689 BB026689
c	48	31.8	22.9	403	2	BB697990	BB697990 BB697990
	49	31.8	22.9	418	5	BP669884	BP669884 BP669884
	50	31.8	22.9	513	9	CE301853	CE301853 tigr-gss-
	51	31.8	22.9	526	2	BB431887	BB431887 BB431887
	52	31.8	22.9	692	8	BZ039148	BZ039148 lka40b01.
	53	31.8	22.9	779	9	CR319158	CR319158 Medicago
	54	31.6	22.7	282	1	AV333759	AV333759 AV333759
c	55	31.6	22.7	475	5	BU094459	BU094459 rf68h04.y
c	56	31.6	22.7	682	4	BI254828	BI254828 602974083
c	57	31.6	22.7	715	9	AG142826	AG142826 Pan trogl
	58	31.4	22.6	825	9	CG929327	CG929327 MBEBC44TF
c	59	31.4	22.6	1050	8	BZ443978	BZ443978 BONII38TR
	60	31.4	22.6	1201	9	CNS00ZYJ	AL098293 Drosophil
	61	31.2	22.4	223	1	AV380299	AV380299 AV380299
	62	31.2	22.4	529	8	AZ090941	AZ090941 RPCI-23-4
	63	31.2	22.4	622	8	AZ555233	AZ555233 RPCI-23-1
	64	31.2	22.4	643	8	AZ266822	AZ266822 RPCI-23-4
c	65	31.2	22.4	684	8	BH454485	BH454485 BOHPH49TR
	66	31	22.3	278	2	BB003106	BB003106 BB003106
c	67	31	22.3	289	1	AA848004	AA848004 od72f12.s
	68	31	22.3	433	1	AA506001	AA506001 ni02c05.s
c	69	31	22.3	623	8	BZ656668	BZ656668 OGAMI06TC
	70	31	22.3	630	1	AV025570	AV025570 AV025570
	71	31	22.3	631	8	AQ609227	AQ609227 HS_5455_A
	72	31	22.3	719	8	BH303592	BH303592 CH230-72H
	73	31	22.3	740	5	BU437903	BU437903 603210649
	74	31	22.3	748	7	CF550786	CF550786 AGENCOURT
c	75	31	22.3	755	9	CG380138	CG380138 OGWKW16TV
c	76	31	22.3	818	7	CK395548	CK395548 AGENCOURT
c	77	31	22.3	867	9	CR007346	CR007346 Forward s
c	78	31	22.3	882	9	CC640698	CC640698 OGLAO03TH
	79	31	22.3	904	9	CC640706	CC640706 OGLAO03TV
c	80	31	22.3	907	9	CG376924	CG376924 OG0AH57TH
	81	31	22.3	925	8	CC377491	CC377491 PUHLA09TB
	82	30.8	22.2	216	2	BB008494	BB008494 BB008494
	83	30.8	22.2	217	2	BB110376	BB110376 BB110376
	84	30.8	22.2	280	2	BB344600	BB344600 BB344600
	85	30.8	22.2	399	6	BY657337	BY657337 BY657337
	86	30.8	22.2	415	2	BB788930	BB788930 BB788930
	87	30.8	22.2	421	5	BY395688	BY395688 BY395688
c	88	30.8	22.2	428	6	CB793924	CB793924 AMGNNUC:N
	89	30.8	22.2	476	5	BQ027415	BQ027415 UI-H-CO0-
	90	30.8	22.2	1033	9	CNS02NAJ	AL205156 Tetraodon
	91	30.6	22.0	268	2	BB007835	BB007835 BB007835
c	92	30.6	22.0	290	6	CB710377	CB710377 AMGNNUC:T
	93	30.6	22.0	305	2	BB045924	BB045924 BB045924
c	94	30.6	22.0	388	6	CB779574	CB779574 AMGNNUC:N
c	95	30.6	22.0	400	6	CB699498	CB699498 AMGNNUC:N
c	96	30.6	22.0	432	2	BE635169	BE635169 uv92f06.x
	97	30.6	22.0	450	1	AJ686825	AJ686825 AJ686825

c 98	30.6	22.0	453	1	AJ574756	AJ574756 AJ574756
99	30.6	22.0	465	2	BE687044	BE687044 uv92f06.y
c 100	30.6	22.0	564	4	BG985735	BG985735 2734 NICH

ALIGNMENTS

RESULT 1
AK082454/c
LOCUS AK082454 3932 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230052F14 product:unclassifiable, full insert sequence.
ACCESSION AK082454
VERSION AK082454.1 GI:26100683
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3932)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
FEATURES Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:C230052F14"
/db_xref="taxon:10090"
/clone="C230052F14"
/tissue_type="cerebellum"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
misc_feature 1. .3932
/note="unclassifiable"
ORIGIN

Query Match 25.0%; Score 34.8; DB 3; Length 3932;
Best Local Similarity 54.8%; Pred. No. 13;
Matches 69; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

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Qy         14 ACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTC 73
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Db       2194 ACTATCTCATTTAAAAGCTCCTTCATCTGTGTGTATATAATGTTTGTGTGAGGATTTTTG 2135

Qy         74 TGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTT 133
              |||| ||| ||||| || || |  || |||  | |  ||   | || |  ||  | || |
Db       2134 TGGTATATGAACTGATTTTCTCAGAATCACATTGAATAAATGTTGATTAGTCAAAGTGGT 2075

Qy        134 AACACA 139
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Db       2074 CAAGCA 2069
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RESULT 2
BY642267
LOCUS BY642267 414 bp mRNA linear EST 15-DEC-2002
DEFINITION BY642267 RIKEN full-length enriched, visual cortex Mus musculus cDNA clone K430350A22 3', mRNA sequence.
ACCESSION BY642267
VERSION BY642267.1 GI:26977449
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 414)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,

Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

MEDLINE 22354683

PUBMED 12466851

COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Michela Fagiolini and Takao K. Hensch (Laboratory for Neuronal Circuit Development Brain Science Institute RIKEN 2-1 Hirosawa,Wako-shi,Saitama 351-0198 Japan) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .414
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="K430350A22"
/tissue_type="visual cortex"
/clone_lib="RIKEN full-length enriched, visual cortex"

ORIGIN

Query Match 24.7%; Score 34.4; DB 6; Length 414;
Best Local Similarity 57.4%; Pred. No. 11;
Matches 62; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

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Qy         31 CTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTT 90
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Db        214 CTGCTCCAGGCTCTTCCTCTTGTGAGCTGTGGTCCCACTGTTCAGATCTCTTCACTGTTT 273

Qy         91 ATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTAACAC 138
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Db        274 TTCTTCAGACCACCCCACACATTGCTTGACAGTCCTTGTTGTCAGCGC 321
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RESULT 3
AV231406
LOCUS AV231406 204 bp mRNA linear EST 15-NOV-2001
DEFINITION AV231406 RIKEN full-length enriched, 0 day neonate skin Mus musculus cDNA clone 4632406L08 3', mRNA sequence.
ACCESSION AV231406
VERSION AV231406.1 GI:6183921
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 204)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Konno,H., et al. 1999)
JOURNAL Unpublished (1999)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y., Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .204
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4632406L08"
/sex="mixed"
/tissue_type="skin"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 0 day neonate skin"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was

primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I"

ORIGIN

Query Match 24.2%; Score 33.6; DB 1; Length 204;
Best Local Similarity 57.7%; Pred. No. 18;
Matches 60; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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Qy         31 CTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTT 90
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Qy         91 ATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTA 134
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Db         70 TTTTTCAGGACACCCCAAACATTGCTTGACAGTCCTTGTTGTCA 113
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RESULT 4
BB775700
LOCUS BB775700 274 bp mRNA linear EST 08-JUL-2003
DEFINITION BB775700 RIKEN full-length enriched, RCB-0559 K-1 . F1 cDNA Mus musculus cDNA clone G430026L09 3', mRNA sequence.
ACCESSION BB775700
VERSION BB775700.1 GI:16936380
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 274)
AUTHORS Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)
JOURNAL Unpublished (2001)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.
FEATURES Location/Qualifiers
source 1. .274
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/mol_type="mRNA"
/strain="DDD"
/db_xref="taxon:10090"
/clone="G430026L09"
/cell_line="RCB-0559 K-1.f1"
/clone_lib="RIKEN full-length enriched, RCB-0559 K-1 . F1 cDNA"
/note="Organ: spleen"
ORIGIN

Query Match 24.2%; Score 33.6; DB 2; Length 274;
Best Local Similarity 57.7%; Pred. No. 18;
Matches 60; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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Qy         31 CTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTT 90
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Db         80 CTGCTCCAGCTCTTCCTCTTCTGAGCTGGTCGTCCCACTTTTCAGATCTCTTCACTGTTT 139

Qy         91 ATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTA 134
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Db        140 TTCTTCAGGACACCCCACACATTGCTTGACAGTCCTTTTTTTCA 183
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RESULT 5
BB094276
LOCUS BB094276 318 bp mRNA linear EST 26-JUN-2000
DEFINITION BB094276 RIKEN full-length enriched, 12 days embryo, embryonic body between diaphragm region and neck Mus musculus cDNA clone 9430045O21 3', mRNA sequence.
ACCESSION BB094276
VERSION BB094276.1 GI:8739310
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 318)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Konno,H., et al.)
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length

cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="9430045O21"
/tissue_type="embryonic body between diaphragm region and neck"
/dev_stage="12 days embryo"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 12 days embryo, embryonic body between diaphragm region and neck"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 370.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI."

ORIGIN

Query Match 24.2%; Score 33.6; DB 2; Length 318;
Best Local Similarity 57.7%; Pred. No. 19;
Matches 60; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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Db        122 CTGCTCCAGGATCTTCTTTTTCTGAGCTGTCGTCCCACTGTTCAGATTTTTTCACTGTTT 181

Qy         91 ATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTA 134
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Db        182 TTCTTCAGGACACCCCACACATTGCTTGACAGTCCTTGTTGTCA 225
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RESULT 6
BB222962
LOCUS BB222962 335 bp mRNA linear EST 01-JUL-2000
DEFINITION BB222962 RIKEN full-length enriched, adult male aorta and vein Mus musculus cDNA clone A530080D21 3', mRNA sequence.
ACCESSION BB222962
VERSION BB222962.1 GI:8891574
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 335)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Konno,H., et al.)
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .335
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="A530080D21"
/sex="male"
/tissue_type="aorta and vein"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male aorta and vein"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN

Query Match 24.2%; Score 33.6; DB 2; Length 335;
Best Local Similarity 57.7%; Pred. No. 19;
Matches 60; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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Qy         31 CTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTT 90
              ||||  ||  ||||| | ||     |  ||     | | |  || | | | || |||||||
Db        139 CTGCTCCAGGCTCTTCTTTTTCTGAGCAGTCGTCCCACTGTTCAGATATTTTCACTGTTT 198

Qy         91 ATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTA 134
                ||  ||   ||||  |  ||  ||| |||  | ||| |||| |
Db        199 TTCTTCAGGACACCCCACACATTGCTTGACATTCCTTGTTGTCA 242
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RESULT 7
BY439440
LOCUS BY439440 448 bp mRNA linear EST 13-DEC-2002
DEFINITION BY439440 RIKEN full-length enriched, pooled tissues, 16 days embryo, etc. Mus musculus cDNA clone I920162D12 3', mRNA sequence.
ACCESSION BY439440
VERSION BY439440.1 GI:26723810
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 448)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 22354683
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
source 1. .448
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="I920162D12"
/clone_lib="RIKEN full-length enriched, pooled tissues, 16 days embryo, etc."
/note="pooled tissues: (dev_stage=16 days embryo,tissue_type=heart,sex=mix),(dev_stage=16 days embryo,tissue_type=kidney,sex=mix),(dev_stage=17 days embryo,tissue_type=heart,sex=mix),(dev_stage=17 days embryo,tissue_type=stomach,sex=mix),(dev_stage=17 days embryo,tissue_type=kidney,sex=mix),(dev_stage=17 days pregnant, adult,tissue_type=amnion,sex=female), (dev_stage=13 days embryo,tissue_type=liver,sex=mix)"
ORIGIN

Query Match 24.2%; Score 33.6; DB 5; Length 448;
Best Local Similarity 61.4%; Pred. No. 20;
Matches 54; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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Qy        47 TCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCAT 106
             ||||| ||      |  | | |  || | | | || ||||||| ||  || ||||||
Db       262 TCTTCTGAGCTGTCGGTCCCACTGTTCAGATCTCTTCACTGTTTTTCTTCAGAGCACCCC 321

Qy       107 AATCAACGCTAGACTGTTCTTATTGTTA 134
             |  ||  ||| ||| || ||| |||| |
Db       322 ACACATTGCTTGACAGTCCTTGTTGTCA 349
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RESULT 8
AZ435636/c
LOCUS AZ435636 570 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0222H14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0222H14 R, genomic survey sequence.
ACCESSION AZ435636
VERSION AZ435636.1 GI:10559649
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 570)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0222 row: H column: 14
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 570.
FEATURES Location/Qualifiers
source 1. .570
/organism="Mus musculus"

/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0222H14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 24.2%; Score 33.6; DB 8; Length 570;
Best Local Similarity 63.8%; Pred. No. 21;
Matches 51; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

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Qy          1 GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGG 60
              |||||| | ||| |   | |||| |  | |    |||| | ||||| |||   ||| |||
Db        216 GTGACTTTAGTCAAGCTAATTAATTTCTCCAATTCTCATCGTCTTTACTTATAAAACAGG 157

Qy         61 GTGACTATTTGTCTGGTTTA 80
              | || | ||||| |   |||
Db        156 GAGAATGTTTGTTTCCCTTA 137
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RESULT 9
BE131381
LOCUS BE131381 590 bp mRNA linear EST 20-FEB-2001
DEFINITION L48-1355T3 Ice plant Lambda Uni-Zap XR expression library, 48 hours NaCl treatment Mesembryanthemum crystallinum cDNA clone L48-1355, mRNA sequence.
ACCESSION BE131381
VERSION BE131381.1 GI:8578744
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 590)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRimers
FORWARD: T7
BACKWARD: T3
Plate: L48-14 row: E column: 7
Seq primer: T3
High quality sequence stop: 350
POLYA=No.
FEATURES Location/Qualifiers
source 1. .590
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="L48-1355"
/tissue_type="Leaf, 48 h 0.4M NaCl"
/dev_stage="Six week old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression library, 48 hours NaCl treatment"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 24.2%; Score 33.6; DB 2; Length 590;
Best Local Similarity 61.4%; Pred. No. 21;
Matches 54; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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Qy         44 TTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCAC 103
              ||||| ||| ||||  ||||||| |  ||     || ||| |   | |||  |||| |||
Db        147 TTTTCATCACAAAGCAGGTGACTTTGGGTTGAAATTCTTATCCCCTAATCAACAAATCAC 206

Qy        104 CATAATCAACGCTAGACTGTTCTTATTG 131
              |  ||  |||  | |    || || |||
Db        207 CTGAAAAAACAGTGGGAGTTTGTTTTTG 234
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RESULT 10
BM658097
LOCUS BM658097 605 bp mRNA linear EST 26-FEB-2002
DEFINITION MCR059H01_69977 Ice plant Lambda Uni-Zap XR expression library, 48 hours NaCl treatment prescreened for removal of highly abundant transcripts Mesembryanthemum crystallinum cDNA clone MCR059H01 5, mRNA sequence.
ACCESSION BM658097
VERSION BM658097.1 GI:18957608
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum (common iceplant)
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 605)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRimers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 059 row: H column: 01
Seq primer: T3 20mer
High quality sequence stop: 605.
FEATURES Location/Qualifiers
source 1. .605
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCR059H01"
/tissue_type="leaf"
/dev_stage="six-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression library, 48 hours NaCl treatment prescreened for removal of highly abundant transcripts"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:

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                    EcoRI; Site_2: XhoI"
ORIGIN

  Query Match            24.2%;  Score 33.6;  DB 4;  Length 605;
  Best Local Similarity  61.4%;  Pred. No. 21;
  Matches   54;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy         44 TTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCAC 103
              ||||| ||| |||| |||||||| |  ||     || ||| |   | |||  |||| |||
Db        153 TTTTCATCACAAAGCAGGTGACTTTGGGTTGAAATTCTTATCCCCTAATCAACAAATCAC 212

Qy        104 CATAATCAACGCTAGACTGTTCTTATTG 131
              |  ||  |||  | |    || || |||
Db        213 CTGAAAAAACAGTGGGAGTTTGTTTTTG 240


RESULT 11
CA835622
LOCUS       CA835622                625 bp    mRNA    linear   EST 12-DEC-2002
DEFINITION  MCS039B06_160752 Ice plant Lambda Uni-Zap XR expression library, 5
            days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2
            AM). Mesembryanthemum crystallinum cDNA clone MCS039B06 5, mRNA
            sequence.
ACCESSION   CA835622
VERSION     CA835622.1  GI:26563387
KEYWORDS    EST.
SOURCE      Mesembryanthemum crystallinum (common iceplant)
  ORGANISM  Mesembryanthemum crystallinum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE   1  (bases 1 to 625)
  AUTHORS   Cushman, J.C.
  TITLE     An expressed sequence tag database for the common ice plant,
            Mesembryanthemum crystallinum
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Cushman JC
            Department of Biochemistry
            University of Nevada
            MS200, Reno, NV 89557-0014, USA
            Tel: 775-784-1918
            Fax: 775-784-1650
            Email: jcushman@unr.edu
            PCR PRimers
            FORWARD: T3 20mer
            BACKWARD: T7 21mer
            Plate: 039  row: B  column: 06
            Seq primer: T3 20mer
            High quality sequence stop: 625.
FEATURES             Location/Qualifiers
     source          1. .625
                     /organism="Mesembryanthemum crystallinum"
                     /mol_type="mRNA"
                     /db_xref="taxon:3544"
                     /clone="MCS039B06"
                     /tissue_type="leaf"
                     /dev_stage="five-week-old"
                     /clone_lib="Ice plant Lambda Uni-Zap XR expression
                     library, 5 days 0.5 M NaCl treatment, Crassulacean acid
                     metabolism, phase I (2 AM)."
                     /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Library construction was performed
                     according to Stratagene's recommended protocol for the
                     Lambda UniZapXR vector and cDNA synthesis kit."
ORIGIN

  Query Match            24.2%;  Score 33.6;  DB 6;  Length 625;
  Best Local Similarity  61.4%;  Pred. No. 21;
  Matches   54;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy         44 TTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCAC 103
              ||||| ||| |||| |||||||| |  ||     || ||| |   | |||  |||| |||
Db        156 TTTTCATCACAAAGCAGGTGACTTTGGGTTGAAATTCTTATCCCCTAATCAACAAATCAC 215

Qy        104 CATAATCAACGCTAGACTGTTCTTATTG 131
              |  ||  |||  | |    || || |||
Db        216 CTGAAAAAACAGTGGGAGTTTGTTTTTG 243


RESULT 12
CA834105
LOCUS       CA834105                633 bp    mRNA    linear   EST 12-DEC-2002
DEFINITION  MCS028H02_153488 Ice plant Lambda Uni-Zap XR expression library, 5
            days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2
            AM). Mesembryanthemum crystallinum cDNA clone MCS028H02 5, mRNA
            sequence.
ACCESSION   CA834105
VERSION     CA834105.1  GI:26561870
KEYWORDS    EST.
SOURCE      Mesembryanthemum crystallinum (common iceplant)
  ORGANISM  Mesembryanthemum crystallinum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE   1  (bases 1 to 633)
  AUTHORS   Cushman, J.C.
  TITLE     An expressed sequence tag database for the common ice plant,
            Mesembryanthemum crystallinum
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Cushman JC
            Department of Biochemistry
            University of Nevada
            MS200, Reno, NV 89557-0014, USA
            Tel: 775-784-1918
            Fax: 775-784-1650
            Email: jcushman@unr.edu
            PCR PRimers
            FORWARD: T3 20mer
            BACKWARD: T7 21mer
            Plate: 028  row: H  column: 02
            Seq primer: T3 20mer
            High quality sequence stop: 633.
FEATURES             Location/Qualifiers
     source          1. .633
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                     /mol_type="mRNA"
                     /db_xref="taxon:3544"
                     /clone="MCS028H02"
                     /tissue_type="leaf"
                     /dev_stage="five-week-old"
                     /clone_lib="Ice plant Lambda Uni-Zap XR expression
                     library, 5 days 0.5 M NaCl treatment, Crassulacean acid
                     metabolism, phase I (2 AM)."
                     /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Library construction was performed
                     according to Stratagene's recommended protocol for the
                     Lambda UniZapXR vector and cDNA synthesis kit."
ORIGIN

  Query Match            24.2%;  Score 33.6;  DB 6;  Length 633;
  Best Local Similarity  61.4%;  Pred. No. 21;
  Matches   54;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy         44 TTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCAC 103
              ||||| ||| |||| |||||||| |  ||     || ||| |   | |||  |||| |||
Db        165 TTTTCATCACAAAGCAGGTGACTTTGGGTTGAAATTCTTATCCCCTAATCAACAAATCAC 224

Qy        104 CATAATCAACGCTAGACTGTTCTTATTG 131
              |  ||  |||  | |    || || |||
Db        225 CTGAAAAAACAGTGGGAGTTTGTTTTTG 252


RESULT 13
BM301497
LOCUS       BM301497                674 bp    mRNA    linear   EST 22-JAN-2002
DEFINITION  MCR046F12_26036 Ice plant Lambda Uni-Zap XR expression library, 48
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            hours NaCl treatment prescreened for removal of highly abundant
            transcripts Mesembryanthemum crystallinum cDNA clone MCR046F12 5,
            mRNA sequence.
ACCESSION   BM301497
VERSION     BM301497.1  GI:18023872
KEYWORDS    EST.
SOURCE      Mesembryanthemum crystallinum (common iceplant)
  ORGANISM  Mesembryanthemum crystallinum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE   1  (bases 1 to 674)
  AUTHORS   Cushman, J.C.
  TITLE     An expressed sequence tag database for the common ice plant,
            Mesembryanthemum crystallinum
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Cushman JC
            Department of Biochemistry
            University of Nevada
            MS200, Reno, NV 89557-0014, USA
            Tel: 775-784-1918
            Fax: 775-784-1650
            Email: jcushman@unr.edu
            PCR PRimers
            FORWARD: T3 20mer
            BACKWARD: T7 21mer
            Plate: 046  row: F  column: 12
            Seq primer: T3 20mer
            High quality sequence stop: 674.
FEATURES             Location/Qualifiers
     source          1. .674
                     /organism="Mesembryanthemum crystallinum"
                     /mol_type="mRNA"
                     /db_xref="taxon:3544"
                     /clone="MCR046F12"
                     /tissue_type="leaf"
                     /dev_stage="six-week-old"
                     /clone_lib="Ice plant Lambda Uni-Zap XR expression
                     library, 48 hours NaCl treatment prescreened for removal
                     of highly abundant transcripts"
                     /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI"
ORIGIN

  Query Match             24.2%;  Score 33.6;  DB 4;  Length 674;
  Best Local Similarity   61.4%;  Pred. No. 22;
  Matches   54;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy         44 TTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCAC 103
              ||||| ||| ||||  ||||||| |  ||     || ||| |   | |||  |||| |||
Db        156 TTTTCATCACAAAGCAGGTGACTTTGGGTTGAAATTCTTATCCCCTAATCAACAAATCAC 215

Qy        104 CATAATCAACGCTAGACTGTTCTTATTG 131
              |  ||  |||  | |    || || |||
Db        216 CTGAAAAAACAGTGGGAGTTTGTTTTTG 243


RESULT 14
BM301422
LOCUS       BM301422                699 bp    mRNA    linear   EST 22-JAN-2002
DEFINITION  MCR045F12_25886 Ice plant Lambda Uni-Zap XR expression library, 48
            hours NaCl treatment prescreened for removal of highly abundant
            transcripts Mesembryanthemum crystallinum cDNA clone MCR045F12 5,
            mRNA sequence.
ACCESSION   BM301422
VERSION     BM301422.1  GI:18023797
KEYWORDS    EST.
SOURCE      Mesembryanthemum crystallinum (common iceplant)
  ORGANISM  Mesembryanthemum crystallinum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE   1  (bases 1 to 699)
  AUTHORS   Cushman, J.C.
  TITLE     An expressed sequence tag database for the common ice plant,
            Mesembryanthemum crystallinum
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Cushman JC
            Department of Biochemistry
            University of Nevada
            MS200, Reno, NV 89557-0014, USA
            Tel: 775-784-1918
            Fax: 775-784-1650
            Email: jcushman@unr.edu
            PCR PRimers
            FORWARD: T3 20mer
            BACKWARD: T7 21mer
            Plate: 045  row: F  column: 12
            Seq primer: T3 20mer
            High quality sequence stop: 699.
FEATURES             Location/Qualifiers
     source          1. .699
                     /organism="Mesembryanthemum crystallinum"
                     /mol_type="mRNA"
                     /db_xref="taxon:3544"
                     /clone="MCR045F12"
                     /tissue_type="leaf"
                     /dev_stage="six-week-old"
                     /clone_lib="Ice plant Lambda Uni-Zap XR expression
                     library, 48 hours NaCl treatment prescreened for removal
                     of highly abundant transcripts"
                     /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI"
ORIGIN

  Query Match             24.2%;  Score 33.6;  DB 4;  Length 699;
  Best Local Similarity   61.4%;  Pred. No. 22;
  Matches   54;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy         44 TTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCAC 103
              ||||| ||| ||||  ||||||| |  ||     || ||| |   | |||  |||| |||
Db        156 TTTTCATCACAAAGCAGGTGACTTTGGGTTGAAATTCTTATCCCCTAATCAACAAATCAC 215

Qy        104 CATAATCAACGCTAGACTGTTCTTATTG 131
              |  ||  |||  | |    || || |||
Db        216 CTGAAAAAACAGTGGGAGTTTGTTTTTG 243


RESULT 15
CR303205
LOCUS       CR303205                746 bp    DNA     linear   GSS 28-FEB-2004
DEFINITION  Medicago truncatula BAC ends cultivar Jemalong A17 of Medicago
            truncatula, genomic survey sequence.
ACCESSION   CR303205
VERSION     CR303205.1  GI:44708225
KEYWORDS    GSS.
SOURCE      Medicago truncatula (barrel medic)
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 746)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-FEB-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
FEATURES             Location/Qualifiers
     source          1. .746
                     /organism="Medicago truncatula"
                     /mol_type="genomic DNA"
                     /cultivar="Jemalong A17"
                     /db_xref="taxon:3880"
                     /clone_lib="MTE1"
                     /note="Vector: pIndigoBAC ; Site_1: EcoRI ; Site_2: EcoRI
```

```
                    ; Debelle F. and Chalhoub B.~Genoscope sequence ID :
                    mte1-21P8FM1"
ORIGIN

  Query Match             24.2%;  Score 33.6;  DB 9;  Length 746;
  Best Local Similarity   61.4%;  Pred. No. 22;
  Matches   54;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy         50 TCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAAT 109
              | |  ||||| ||||  ||| |||    |  ||  ||  | ||||||| |||| | ||  ||
Db        517 TGATTAAGAGAGTGATGATTAGTCAATTACATACACAATATATCCCAAAAGGAGCACCAT 576

Qy        110 CAACGCTAGACTGTTCTTATTGTTAACA 137
              ||| | || ||| |    |   | ||||
Db        577 CAATGATATACTATATCCAAAATGAACA 604


RESULT 16
BE035174
LOCUS       BE035174                863 bp    mRNA    linear   EST 07-JUN-2000
DEFINITION  MO22B09 MO Mesembryanthemum crystallinum cDNA 5' similar to
            drought-induced protein di19, mRNA sequence.
ACCESSION   BE035174
VERSION     BE035174.1  GI:8330298
KEYWORDS    EST.
SOURCE      Mesembryanthemum crystallinum (common iceplant)
  ORGANISM  Mesembryanthemum crystallinum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE   1  (bases 1 to 863)
  AUTHORS   Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M.,
            Ferrea,H., Kawasaki,S., McCollough,A., Michalowski,C.B.,
            Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R.
  TITLE     Functional Genomics of Plant Stress Tolerance
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Michalowski,C.B.
            University of Arizona
            Bio Sciences West room 513, Tucson, AZ 85721, USA
            Tel: 520-621-7982
            Fax: 520-621-1697
            Email: cbm@u.arizona.edu
            An open reading frame exists.
FEATURES             Location/Qualifiers
     source          1. .863
                     /organism="Mesembryanthemum crystallinum"
                     /mol_type="mRNA"
                     /db_xref="taxon:3544"
                     /tissue_type="apical meristem and leaf primordia"
                     /dev_stage="5 weeks"
                     /clone_lib="MO"
                     /note="no stress"
ORIGIN

  Query Match             24.2%;  Score 33.6;  DB 2;  Length 863;
  Best Local Similarity   61.4%;  Pred. No. 23;
  Matches   54;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy         44 TTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCAC 103
              |||||  ||| ||||  ||||||| |  ||     || ||| |   | |||  |||| |||
Db        168 TTTTCATCACAAAGCAGGTGACTTTGGGTTGAAATTCTTATCCCCTAATCAACAAATCAC 227

Qy        104 CATAATCAACGCTAGACTGTTCTTATTG 131
              |  ||  |||  | |    || || |||
Db        228 CTGAAAAAACAGTGGGAGTTTGTTTTTG 255


RESULT 17
CR308064
LOCUS       CR308064                866 bp    DNA     linear   GSS 01-MAR-2004
DEFINITION  Medicago truncatula BAC ends cultivar Jemalong A17 of Medicago
            truncatula, genomic survey sequence.
ACCESSION   CR308064
VERSION     CR308064.1  GI:44854208
KEYWORDS    GSS.
SOURCE      Medicago truncatula (barrel medic)
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 866)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-FEB-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
FEATURES             Location/Qualifiers
     source          1. .866
                     /organism="Medicago truncatula"
                     /mol_type="genomic DNA"
                     /cultivar="Jemalong A17"
                     /db_xref="taxon:3880"
                     /clone_lib="MTE1"
                     /note="Vector: pIndigoBAC ; Site_1: EcoRI ; Site_2: EcoRI
                     ; Debelle F. and Chalhoub B.~Genoscope sequence ID :
                     mte1-29K6FM1"
ORIGIN

  Query Match             24.2%;  Score 33.6;  DB 9;  Length 866;
  Best Local Similarity   61.4%;  Pred. No. 23;
  Matches   54;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy         50 TCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAAT 109
              | |  ||||| ||||  ||| |||    |  ||  ||  | ||||||| |||| | ||  ||
Db        516 TGATTAAGAGAGTGATGATTAGTCAATTACATACACAATATATCCCAAAAGGAGCACCAT 575

Qy        110 CAACGCTAGACTGTTCTTATTGTTAACA 137
              ||| | || ||| |    |   | ||||
Db        576 CAATGATATACTATATCCAAAATGAACA 603


RESULT 18
CG952370
LOCUS       CG952370                889 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  MBEAT30TR mth2 Medicago truncatula genomic clone 15F12, genomic
            survey sequence.
ACCESSION   CG952370
VERSION     CG952370.1  GI:39864834
KEYWORDS    GSS.
SOURCE      Medicago truncatula (barrel medic)
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 889)
  AUTHORS   Town,C.D., Shetty,J., Koo,H. and Feldblyum,T.F.
  TITLE     Sequencing of BAC ends from Medicago truncatula
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: MBEAT30TF
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            Seq primer: CAGGAAACAGCTATGACC
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .889
                     /organism="Medicago truncatula"
                     /mol_type="genomic DNA"
                     /cultivar="genotype A17"
                     /db_xref="taxon:3880"
                     /clone="15F12"
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                     /clone_lib="mth2"
                     /note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                     HindIII; Cook, D.R. and Kim, D.J, unpublished"
ORIGIN

  Query Match             24.2%;  Score 33.6;  DB 9;  Length 889;
  Best Local Similarity   63.8%;  Pred. No. 23;
  Matches   51;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          44 TTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCAC 103
               | ||  | |  ||||| |||| ||| |||  |  ||  ||  | |||||| |||  |
Db         356 TATTGATGATTAAGAGAGTGATGATTAGTCAATTACATACACAATATATCCCAAAAAGAG 415

Qy         104 CATAATCAACGCTAGACTGT 123
               ||| ||||| | || ||| |
Db         416 CATCATCAATGATATACTAT 435


RESULT 19
BE037111
LOCUS       BE037111                1192 bp    mRNA    linear   EST 07-JUN-2000
DEFINITION  MP15B07 MP Mesembryanthemum crystallinum cDNA 5' similar to
            drought-induced protein di19, mRNA sequence.
ACCESSION   BE037111
VERSION     BE037111.1  GI:8332127
KEYWORDS    EST.
SOURCE      Mesembryanthemum crystallinum (common iceplant)
  ORGANISM  Mesembryanthemum crystallinum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE   1  (bases 1 to 1192)
  AUTHORS   Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M.,
            Ferrea,H., Kawasaki,S., McCollough,A., Michalowski,C.B.,
            Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R.
  TITLE     Functional Genomics of Plant Stress Tolerance
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Michalowski,C.B.
            University of Arizona
            Bio Sciences West room 513, Tucson, AZ 85721, USA
            Tel: 520-621-7982
            Fax: 520-621-1697
            Email: cbm@u.arizona.edu
            Insert Length: 1   Std Error: 0.00.
FEATURES             Location/Qualifiers
     source          1. .1192
                     /organism="Mesembryanthemum crystallinum"
                     /mol_type="mRNA"
                     /db_xref="taxon:3544"
                     /tissue_type="apical meristem and leaf primordia"
                     /dev_stage="6 weeks"
                     /clone_lib="MP"
                     /note="3 d 500mM NaCl"
ORIGIN

  Query Match             24.2%;  Score 33.6;  DB 2;  Length 1192;
  Best Local Similarity   61.4%;  Pred. No. 24;
  Matches   54;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy          44 TTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCAC 103
               |||||  |||  ||||  ||||||| |  ||     || |||  |   | |||  |||| |||
Db         172 TTTTCATCACAAAGCAGGTGACTTTGGGTTGAAATTCTTATCCCCTAATCAACAAATCAC 231

Qy         104 CATAATCAACGCTAGACTGTTCTTATTG 131
               |  ||  |||  | |    || || |||
Db         232 CTGAAAAAACAGTGGGAGTTTGTTTTTG 259


RESULT 20
AQ830244/c
LOCUS       AQ830244                 521 bp    DNA     linear   GSS 27-AUG-1999
DEFINITION  HS_4825_B2_G12_SP6E CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=4825 Col=24 Row=N, genomic survey
            sequence.
ACCESSION   AQ830244
VERSION     AQ830244.1  GI:5796306
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 521)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
   PUBMED   10449764
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones may be purchased from Research Genetics (info@resgen.com).
            BAC end Web Server: http://www.htsc.washington.edu
            Plate: 4825  row: N  column: 24
            Seq primer: T7
            Class: BAC ends
            High quality sequence stop: 521.
FEATURES             Location/Qualifiers
     source          1. .521
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="Plate=4825 Col=24 Row=N"
                     /sex="male"
                     /clone_lib="CIT Approved Human Genomic Sperm Library D"
                     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                     E-Coli DH10B"
ORIGIN

  Query Match             24.0%;  Score 33.4;  DB 8;  Length 521;
  Best Local Similarity   54.5%;  Pred. No. 24;
  Matches   67;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy           2 TGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGG 61
               |||||||| | |   ||| || |  |  | | ||||   |||||| |  | ||| ||||
Db         407 TGACTCTGGGCAAGTCACTAAACTTGTCTCAGTCTCAATTTCTTTTTTAGAAAAATAGGG 348

Qy          62 TGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGACT 121
                 ||| |  |                |||||  |         |||  |||||| || || | |
Db         347 ATGCTAATAATAAAAAAGCAGCACTGTCTCAAGGATTAGCTACATAATTAATGCAAAATG 288

Qy         122 GTT 124
                ||
Db         287 CTT 285


RESULT 21
AG308530
LOCUS       AG308530                 728 bp    DNA     linear   GSS 02-JUN-2004
DEFINITION  Mus musculus molossinus DNA, clone:MSMg01-090D23.TJ, genomic survey
            sequence.
ACCESSION   AG308530
VERSION     AG308530.1  GI:47881484
KEYWORDS    GSS.
SOURCE      Mus musculus molossinus
  ORGANISM  Mus musculus molossinus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
```

```
  TITLE     BAC end Sequences of Library MSMg01
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 728)
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the mouse BAC library MSMg01. For BAC
            library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
            Tsukuba Institude, Bio Resource Center,
            The Institute of Physical and Chemical Research (RIKEN) 3-1-1
            Koyadai, Tsukuba, 305-0074 Japan
            phone: 81-298-36-9189, fax: 81-298-36-9199
            e-mail: abe@rtc.riken.jp
            PRIMERS
            Sequencing : TJ
            LIBRARY
            Vector     : pBACe3.6
            R.Site 1   : EcoRI
            R.Site 2   : EcoRI.
FEATURES              Location/Qualifiers
     source           1. .728
                      /organism="Mus musculus molossinus"
                      /mol_type="genomic DNA"
                      /sub_species="molossinus"
                      /db_xref="taxon:57486"
                      /clone="MSMg01-090D23.TJ"
                      /sex="male"
                      /tissue_type="mixture of kidney and spleen"
                      /clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN

  Query Match             24.0%;  Score 33.4;  DB 9;  Length 728;
  Best Local Similarity   58.6%;  Pred. No. 25;
  Matches   58;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy         39 CCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAA 98
              |||||||| ||| ||  |||    |   | | | ||    | |||   ||||  | || |
Db        216 CCCTCTTTACTTTAGCTAGATCATACTTTTATATCACAGTGATTTTGTGTTGTTTCCTAT 275

Qy         99 AGCACCATAATCAACGCTAGACTGTTCTTATTGTTAACA 137
              ||||| | |    || | || || | ||| |  ||| ||
Db        276 AGCACAAAATATTACTCAAGCCTTTACTTCTAATTATCA 314


RESULT 22
CA791309/c
LOCUS       CA791309                957 bp    mRNA    linear   EST 04-DEC-2002
DEFINITION  AGENCOURT_10304652 NICHD_XGC_Emb1 Xenopus laevis cDNA clone
            IMAGE:5161843 5', mRNA sequence.
ACCESSION   CA791309
VERSION     CA791309.1  GI:26038076
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 957)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11401  row: j  column: 20
            High quality sequence stop: 360.
FEATURES              Location/Qualifiers
     source           1. .957
                      /organism="Xenopus laevis"
                      /mol_type="mRNA"
                      /db_xref="taxon:8355"
                      /clone="IMAGE:5161843"
                      /tissue_type="embryo (stage 10)"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NICHD_XGC_Emb1"
                      /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI;
                      Cloned unidirectionally. Primer: Oligo dT. Average insert
                      size 1.55 kb. Constructed by Life Technologies. Note: This
                      is a Xenopus Gene Collection (XGC) library."
ORIGIN

  Query Match             24.0%;  Score 33.4;  DB 6;  Length 957;
  Best Local Similarity   72.9%;  Pred. No. 26;
  Matches   43;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         21 TAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTT 79
              |||||  |||| | |   || | |||| || |||||| ||| ||| ||||||  |||||
Db        917 TAAATTTTGCCGGGCCAGCCGTTTTTTTTAAGAAAGGGGGGGACAATTTGTGGGGTTT 859


RESULT 23
BB004186
LOCUS       BB004186                205 bp    mRNA    linear   EST 22-JUN-2000
DEFINITION  BB004186 RIKEN full-length enriched, 10 day neonate skin Mus
            musculus cDNA clone 4732458O14 3', mRNA sequence.
ACCESSION   BB004186
VERSION     BB004186.1  GI:8093634
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 205)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
            Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,
            Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,
            Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,
            Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A.,
            Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A.,
            Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A.,
            Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
            Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
            Okazaki,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
```

system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .205
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4732458O14"
/sex="mixed"
/tissue_type="skin"
/dev_stage="10 days neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 10 day neonate skin"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I"

ORIGIN

Query Match 23.9%; Score 33.2; DB 2; Length 205;
Best Local Similarity 57.8%; Pred. No. 23;
Matches 59; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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Qy         35 CTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCC 94
              |||  |||||| |  |    |  ||     | | || || | | | || |||||||  ||
Db         13 CTCCACCTCTTCTTGTTCTGAGCAGTTCTCCCACTTTTCAGATCTTTTCACTGTTTTTCT 72

Qy         95 CCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTAAC 136
                ||   ||||  |  ||  ||| ||| | ||| |||| | |
Db         73 TCAGGACACCCCACACATTGCTTGACATTCCTTGTTGTCACC 114
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RESULT 24
BZ915818
LOCUS BZ915818 467 bp DNA linear GSS 12-JUN-2003
DEFINITION CH240_59A23.TV CHORI-240 Bos taurus genomic clone CH240_59A23, genomic survey sequence.
ACCESSION BZ915818
VERSION BZ915818.1 GI:31641204
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 467)
AUTHORS Larkin,D.M., Everts-van der Wind,A., Rebeiz,M., Schweitzer,P., Bachman,S., Green,S., Campos,E.J., Benson,L.D., Edwards,J., Liu,L., Womack,J.E., de Jong,P.J. and Lewin,H.A.
TITLE A Cattle-Human Comparative Map Built with Cattle BAC-ends and Human Genome Sequence
JOURNAL Unpublished (2003)
COMMENT Contact: Harris Lewin
Department of Animal Sciences
University of Illinois at Urbana Champaign
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by by University of Illinois at Urbana Champaign, USA with funds provided by grant No. AG202-34480-11828 from USDA-CSREES and AG99-35205-8534 from USDA/NRI (Livestock Genome Sequencing Initiative)
Plate: 59 row: A column: 23
Seq primer: T7
Class: BAC ends.

FEATURES Location/Qualifiers
source 1. .467
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_59A23"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 23.7%; Score 33; DB 8; Length 467;
Best Local Similarity 58.8%; Pred. No. 31;
Matches 57; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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Qy         18 ACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGT 77
              |||||  |  ||  | || ||||   |  | |  | |||||  || |   ||| | ||
Db         46 ACTTATTTGCTGGATTCCCCACCAGATGATTTCAACAAAGACTGTAAAGTTTTTTGTGAG 105

Qy         78 TTATTAACTGTTTATCCCCAAAGCACCATAATCAACG 114
              ||||||  |||   || | |||  || || | ||| |
Db        106 TTATTATATGTAACTCACAAAATAACAATGAGCAAAG 142
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RESULT 25
AV336201
LOCUS AV336201 206 bp mRNA linear EST 11-NOV-1999
DEFINITION AV336201 RIKEN full-length enriched, adult male medulla oblongata Mus musculus cDNA clone 6330583F07 3', mRNA sequence.
ACCESSION AV336201
VERSION AV336201.1 GI:6376253
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 206)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Konno,H., et al. 1999)
JOURNAL Unpublished (1999)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y., Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .206
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="6330583F07"
/sex="male"
/tissue_type="medulla oblongata"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male medulla oblongata"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"

ORIGIN

Query Match 23.6%; Score 32.8; DB 1; Length 206;
Best Local Similarity 56.5%; Pred. No. 31;
Matches 61; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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Qy         27 ATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACT 86
              ||  ||| |||  || || |  |    |         | | || || | ||||||||||
Db          6 ATAGATGCTTCAGGCTTTTCTTCTTCTGAGCTTTTCTCCCACTTTTCAGATTTATTAACT 65

Qy         87 GTTTATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTA 134
              |||| |   ||   ||||  |  ||  ||| |||  | ||| |||| |
Db         66 GTTTTTTTTCAGGACACCCCACACATTGCTTGACATTCCTTGTTGTCA 113
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RESULT 26
BZ035953/c
LOCUS BZ035953 690 bp DNA linear GSS 09-OCT-2002
DEFINITION oeh99d03.g1 B.oleracea002 Brassica oleracea genomic, genomic survey sequence.
ACCESSION BZ035953
VERSION BZ035953.1 GI:23614280
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 690)
AUTHORS Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T., Nash,W., Rabinowicz,P.D. and Wilson,R.K.
TITLE Whole genome shotgun reads from Brassica oleracea
JOURNAL Unpublished (2002)
COMMENT Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: oeh99 row: d column: 03
Seq primer: -28RPpOT reverse
Class: shotgun
High quality sequence start: 17
High quality sequence stop: 551.

FEATURES Location/Qualifiers
source 1. .690
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."

ORIGIN

Query Match 23.6%; Score 32.8; DB 8; Length 690;
Best Local Similarity 56.5%; Pred. No. 38;
Matches 61; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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Qy         30 CCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTT 89
              ||  || || |||| ||  || | ||||||  |  || ||||||     || | |
Db        610 CCGACCACATCCTCCTTGTTTGAAAAAGAGTTTTCCTTTTTGTCAAAAACATGATCATAA 551

Qy         90 TATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTAACA 137
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Db        550 TATATATATATATATATAATCAAAGCTACAGGTTTCTGACAAGTACCA 503
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RESULT 27
BB230680
LOCUS BB230680 252 bp mRNA linear EST 04-JUL-2000
DEFINITION BB230680 RIKEN full-length enriched, 3 days neonate thymus Mus musculus cDNA clone A630028L21 3', mRNA sequence.
ACCESSION BB230680
VERSION BB230680.1 GI:8910593
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 252)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A.,

Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
source 1. .252
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="A630028L21"
/tissue_type="thymus"
/dev_stage="3 days neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 3 days neonate thymus"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
ORIGIN

Query Match 23.3%; Score 32.4; DB 2; Length 252;
Best Local Similarity 56.6%; Pred. No. 42;
Matches 60; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

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Qy          31 CTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTT 90
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Db          56 CTGCTCCAGGCTCTTCCTCTTCTGACCTTTCTTCCCACTGTTCAGATTTCTTCACTGTTT 115

Qy          91 ATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTAAC 136
                 ||  ||   ||||  |  ||  ||| ||| || ||| |||| | |
Db         116 TTCTTCAGGACACCCCACACATTGCTTGACAGTCCTTGTTGTCACC 161
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RESULT 28
BB118576
LOCUS BB118576 270 bp mRNA linear EST 27-JUN-2000
DEFINITION BB118576 RIKEN full-length enriched, adult male urinary bladder Mus musculus cDNA clone 9530066I16 3', mRNA sequence.
ACCESSION BB118576
VERSION BB118576.1 GI:8771144
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 270)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Konno,H., et al.)
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
source 1. .270
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="9530066I16"
/sex="male"
/tissue_type="urinary bladder"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male urinary bladder"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 370.0. Second strand cDNA was prepared with the primer adapter of

sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN

Query Match 23.3%; Score 32.4; DB 2; Length 270;
Best Local Similarity 56.6%; Pred. No. 42;
Matches 60; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

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Qy         31 CTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTT 90
              ||||  ||  ||||| | ||     |  |    |  | | || || | ||| || ||| |||
Db         76 CTGCTCCAGGCTCTTCTTTTTTTGAGCATTTTTCCCACTTTTCAGATTTTTTCACTTTTT 135

Qy         91 ATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTAAC 136
                |   ||   ||||  |  ||  ||| |||  | ||  |||| | |
Db        136 TTTTTCAGGACACCCCACACATTGCTTGACATTCCTCGTTGTCACC 181
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RESULT 29
BY480819
LOCUS BY480819 533 bp mRNA linear EST 02-JAN-2003
DEFINITION BY480819 RIKEN full-length enriched, B16 F10Y cells Mus musculus cDNA clone G370145K21 3', mRNA sequence.
ACCESSION BY480819
VERSION BY480819.1 GI:26815198
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 533)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 22354683
PUBMED 12466851
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The Institute of Physical and Chemical Research (RIKEN)
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Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Cells were provided by Drs. William J Pavan, Stacie Loftus, and Denise Larson (Division of Intramural Research Genetic Disease Research Branch National Human Genome Reseach Institute, National Institutes of Health (NIH) Building: 49, Room 4A82 49 Convent Drive MSC 4472 Bethesda, Maryland U.S.A) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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REFERENCE 1 (bases 1 to 906)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

```
  MEDLINE   99380589
   PUBMED   10449764
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones may be purchased from Research Genetics (info@resgen.com).
            BAC end Web Server: http://www.htsc.washington.edu
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Db        690 CCCCCTCCTCTTTTTTTAAAAAAGAGGGTTTGTATTTTTTTTTTTTTTTTTTTTTTCTC 749

Qy         94 CCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
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